

Six fractions were collected, dried, suspended in PBS and tested individually in *M. tuberculosis*-infected guinea pigs for induction of delayed type hypersensitivity (DTH) reaction. One fraction was found to induce a strong DTH reaction and was subsequently fractionated further by RP-HPLC on a microbore Vydac C18 column (Cat. No. 218TP5115) in a Perkin Elmer/Applied Biosystems Division Model 172 HPLC. Fractions were eluted with a linear gradient from 5-100% buffer (0.05% TFA in acetonitrile) with a flow rate of 80 μ l/minute. Eluent was monitored at 215 nm. Eight fractions were collected and tested for induction of DTH in *M. tuberculosis*-infected guinea pigs. One fraction was found to induce strong DTH of about 16 mm induration. The other fractions did not induce detectable DTH. The positive fraction was submitted to SDS-PAGE gel electrophoresis and found to contain a single protein band of approximately 12 kD molecular weight.

This polypeptide, herein after referred to as DPPD, was sequenced from the amino terminal using a Perkin Elmer/Applied Biosystems Division Procise 492 protein sequencer as described above and found to have the N-terminal sequence shown in SEQ ID No.: 129. Comparison of this sequence with known sequences in the gene bank as described above revealed no known homologies. Four cyanogen bromide fragments of DPPD were isolated and found to have the sequences shown in SEQ ID Nos.: 130-133. A subsequent search of the *M. tuberculosis* genome database released by the Institute for Genomic Research revealed a match of the DPPD partial amino acid sequence with a sequence present within the *M. tuberculosis* cosmid MTY21C12. An open reading frame of 336 bp was identified. The full-length DNA sequence for DPPD is provided in SEQ ID NO: 240, with the corresponding full-length amino acid sequence being provided in SEQ ID NO: 241.

The ability of the antigen DPPD to stimulate human PBMC to proliferate and to produce IFN- γ was assayed as described in Example 1. As shown in Table 9, DPPD was found to stimulate proliferation and elicit production of large quantities of IFN- γ ; more than that elicited by commercial PPD.

TABLE 9
RESULTS OF PROLIFERATION AND INTERFERON- γ ASSAYS TO DPPD

PBMC Donor	Stimulator	Proliferation (CPM)	IFN- γ (OD ₁₈₆)
A	Medium	1,089	0.17
	PPD (commercial)	8,394	1.29
	DPPD	13,451	2.21
B	Medium	450	0.09
	PPD (commercial)	3,929	1.26
	DPPD	6,184	1.49
C	Medium	541	0.11
	PPD (commercial)	8,907	0.76
	DPPD	23,024	>2.70

EXAMPLE 5

USE OF SERA FROM TUBERCULOSIS-INFECTED MONKEYS TO IDENTIFY DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS

Genomic DNA was isolated from *M. tuberculosis* Erdman strain, randomly sheared and used to construct an expression library employing the Lambda ZAP expression system (Stratagene, La Jolla, CA). Serum samples were obtained from a cynomolgous monkey 18, 33, 51 and 56 days following infection with *M. tuberculosis* Erdman strain. These samples were pooled and used to screen the *M. tuberculosis* genomic DNA expression library using the procedure described above in Example 3C.

Twenty clones were purified. The determined 5' DNA sequences for the clones referred to as MO-1, MO-2, MO-4, MO-8, MO-9, MO-26, MO-28, MO-29, MO-30, MO-34 and MO-35 are provided in SEQ ID NO: 215-225, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 226-236. The full-length DNA sequence of the clone MO-10 is provided in SEQ ID NO: 237, with the corresponding

predicted amino acid sequence being provided in SEQ ID NO: 238. The 3' DNA sequence for the clone MO-27 is provided in SEQ ID NO: 239.

Clones MO-1, MO-30 and MO-35 were found to show a high degree of relatedness and showed some homology to a previously identified unknown *M. tuberculosis* sequence and to cosmid MTC1237. MO-2 was found to show some homology to aspartokinase from *M. tuberculosis*. Clones MO-3, MO-7 and MO-27 were found to be identical and to show a high degree of relatedness to MO-5. All four of these clones showed some homology to *M. tuberculosis* heat shock protein 70. MO-27 was found to show some homology to *M. tuberculosis* cosmid MTCY339. MO-4 and MO-34 were found to show some homology to cosmid SCY21B4 and *M. smegmatis* integration host factor, and were both found to show some homology to a previously identified, unknown *M. tuberculosis* sequence. MO-6 was found to show some homology to *M. tuberculosis* heat shock protein 65. MO-8, MO-9, MO-10, MO-26 and MO-29 were found to be highly related to each other and to show some homology to *M. tuberculosis* dihydroilipamide succinyltransferase. MO-28, MO-31 and MO-32 were found to be identical and to show some homology to a previously identified *M. tuberculosis* protein. MO-33 was found to show some homology to a previously identified 14 kDa *M. tuberculosis* heat shock protein.

Further studies using the above protocol resulted in the isolation of an additional four clones, hereinafter referred to as MO-12, MO-13, MO-19 and MO-39. The determined 3' cDNA sequences for these clones are provided in SEQ ID NO: 295-298, respectively, with the corresponding predicted protein sequences being provided in SEQ ID NO: 299-302, respectively. Comparison of these sequences with those in the gene bank as described above revealed no significant homologies to MO-39. MO-12, MO-13 and MO-19 were found to show some homologies to unknown sequences previously isolated from *M. tuberculosis*.

EXAMPLE 6

ISOLATION OF DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS BY SCREENING OF A NOVEL EXPRESSION LIBRARY

This example illustrates isolation of DNA sequences encoding *M. tuberculosis* antigens by screening of a novel expression library with sera from *M. tuberculosis*-infected patients that were shown to be unreactive with a panel of the recombinant *M. tuberculosis* antigens TbRa11, TbRa3, Tb38-1, TbH4, TbF and 38 kD.

Genomic DNA from *M. tuberculosis* Erdman strain was randomly sheared to an average size of 2 kb, and blunt ended with Klenow polymerase, followed by the addition of EcoRI adaptors. The insert was subsequently ligated into the Screen phage vector (Novagen, Madison, WI) and packaged *in vitro* using the PhageMaker extract (Novagen). The resulting library was screened with sera from several *M. tuberculosis* donors that had been shown to be negative on a panel of previously identified *M. tuberculosis* antigens as described above in Example 3B.

A total of 22 different clones were isolated. By comparison, screening of the λ Zap library described above using the same sera did not result in any positive hits. One of the clones was found to represent TbRa11, described above. The determined 5' cDNA sequences for 19 of the remaining 21 clones (hereinafter referred to as Erdsn1, Erdsn2, Erdsn4-Erdsn10, Erdsn12-18, Erdsn21-Erdsn23 and Erdsn25) are provided in SEQ ID NO: 303-322, respectively, with the determined 3' cDNA sequences for Erdsn1, Erdsn2, Erdsn4, Erdsn5, Erdsn7-Erdsn10, Erdsn12-18, Erdsn21-Erdsn23 and Erdsn25 being provided in SEQ ID NO: 323-341, respectively. The complete cDNA insert sequence for the clone Erdsn24 is provided in SEQ ID NO: 342. Comparison of the determined cDNA sequences with those in the gene bank revealed no significant homologies to the sequences provided in SEQ ID NO: 309, 316, 318-320, 322, 324, 328, 329, 333, 335, 337, 339 and 341. The sequences of SEQ ID NO: 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342 were found to show some homology to unknown sequences previously identified in *M. tuberculosis*.

EXAMPLE 7

ISOLATION OF SOLUBLE *M. TUBERCULOSIS* ANTIGENS

USING MASS SPECTROMETRY

This example illustrates the use of mass spectrometry to identify soluble *M. tuberculosis* antigens.

In a first approach, *M. tuberculosis* culture filtrate was screened by Western analysis using serum from a tuberculosis-infected individual. The reactive bands were excised from a silver stained gel and the amino acid sequences determined by mass spectrometry. The determined amino acid sequence for one of the isolated antigens is provided in SEQ ID NO: 343. Comparison of this sequence with those in the gene bank revealed homology to the 85b precursor antigen previously identified in *M. tuberculosis*.

In a second approach, the high molecular weight region of *M. tuberculosis* culture supernatant was studied. This area may contain immunodominant antigens which may be useful in the diagnosis of *M. tuberculosis* infection. Two known monoclonal antibodies, IT42 and IT57 (available from the Center for Disease Control, Atlanta, GA), show reactivity by Western analysis to antigens in this vicinity, although the identity of the antigens remains unknown. In addition, unknown high-molecular weight proteins have been described as containing a surrogate marker for *M. tuberculosis* infection in HIV-positive individuals (*Int. Infect. Dis.*, 176:133-143, 1997). To determine the identity of these antigens, two-dimensional gel electrophoresis and two-dimensional Western analysis were performed using the antibodies IT57 and IT42. Five protein spots in the high molecular weight region were identified, individually excised, enzymatically digested and subjected to mass spectrometric analysis.

The determined amino acid sequences for three of these spots (referred to as spots 1, 2 and 4) are provided in SEQ ID NO: 344, 345-346 and 347, respectively. Comparison of these sequences with those in the gene bank revealed that spot 1 is the previously identified Pck-1, a phosphoenolpyruvate kinase. The two sequences isolated from spot 2 were determined to be from two DNAs, previously identified in *M. tuberculosis* as heat shock proteins. Spot 4 was determined to be the previously identified *M. tuberculosis* protein Kat G. To the best of the inventors' knowledge, neither Pck-1 nor the two DNAs have previously been shown to have utility in the diagnosis of *M. tuberculosis* infection.

EXAMPLE 8

USE OF REPRESENTATIVE ANTIGENS FOR DIAGNOSIS OF TUBERCULOSIS

This example illustrates the effectiveness of several representative polypeptides in skin tests for the diagnosis of *M. tuberculosis* infection.

Individuals were injected intradermally with 100 μ l of either PBS or PBS plus Tween 20™ containing either 0.1 μ g of protein (for TbH-9 and TbRa35) or 1.0 μ g of protein (for TbRa38-1). Induration was measured between 5-7 days after injection, with a response of 5 mm or greater being considered positive. Of the 20 individuals tested, 2 were PPD negative and 18 were PPD positive. Of the PPD positive individuals, 3 had active tuberculosis, 3 had been previously infected with tuberculosis and 9 were healthy. In a second study, 13 PPD positive individuals were tested with 0.1 μ g TbRa11 in either PBS or PBS plus Tween 20™ as described above. The results of both studies are shown in Table 10.

TABLE 10
RESULTS OF DTH TESTING WITH REPRESENTATIVE ANTIGENS

	TbH-9 Pos/Total	Tb38-1 Pos/Total	TbRa35 Pos/Total	Cumulative Pos/Total	TbRa11 Pos/Total
PPD negative	0/2	0/2	0/2	0/2	
PPD positive					
healthy	5/9	4/9	4/9	6/9	1/4
prior TB	3/5	2/5	2/5	4/5	3/3
active	3/4	3/4	0/4	4/4	1/4
TOTAL	11/18	9/18	6/18	14/18	5/13

EXAMPLE 9

SYNTHESIS OF SYNTHETIC POLYPEPTIDES

Polypeptides may be synthesized on a Millipore 9050 peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N',N''-tetramethyluronium

hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray mass spectrometry and by amino acid analysis.

EXAMPLE 10

PREPARATION AND CHARACTERIZATION OF *M. TUBERCULOSIS* FUSION PROTEINS

A fusion protein containing TbRa3, the 38 kD antigen and Tb38-1 was prepared as follows.

Each of the DNA constructs TbRa3, 38 kD and Tb38-1 were modified by PCR in order to facilitate their fusion and the subsequent expression of the fusion protein TbRa3-38 kD-Tb38-1. TbRa3, 38 kD and Tb38-1 DNA was used to perform PCR using the primers PDM-64 and PDM-65 (SEQ ID NO: 146 and 147), PDM-57 and PDM-58 (SEQ ID NO: 148 and 149), and PDM-69 and PDM-60 (SEQ ID NO: 150 and 151), respectively. In each case, the DNA amplification was performed using 10 μ l 10X Pfu buffer, 2 μ l 10 mM dNTPs, 2 μ l each of the PCR primers at 10 μ M concentration, 81.5 μ l water, 1.5 μ l Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 μ l DNA at either 70 ng/ μ l (for TbRa3) or 50 ng/ μ l (for 38 kD and Tb38-1). For TbRa3, denaturation at 94°C was performed for 2 min, followed by 40 cycles of 96°C for 15 sec and 72°C for 1 min, and lastly by 72°C for 4 min. For 38 kD, denaturation at 96°C was performed for 2 min, followed by 40 cycles of 96°C for 30 sec, 68°C for 15 sec and 72°C for 3 min, and finally by 72°C for 4 min. For Tb38-1 denaturation at 94°C for 2 min was followed by 10 cycles of 96°C for 15 sec, 68°C for 15 sec and 72°C for

1.5 min, 30 cycles of 96°C for 15 sec, 64°C for 15 sec and 72°C for 1.5, and finally by 72°C for 4 min.

The TbRa3 PCR fragment was digested with NdeI and EcoRI and cloned directly into pT7⁺L2 IL 1 vector using NdeI and EcoRI sites. The 38 kD PCR fragment was digested with Sse8387I, treated with T4 DNA polymerase to make blunt ends and then digested with EcoRI for direct cloning into the pT7⁺L2Ra3-1 vector which was digested with StuI and EcoRI. The 38-1 PCR fragment was digested with Eco47III and EcoRI and directly subcloned into pT7⁺L2Ra3/38kD-17 digested with the same enzymes. The whole fusion was then transferred to pET28b - using NdeI and EcoRI sites. The fusion construct was confirmed by DNA sequencing.

The expression construct was transformed into BLR pLys S *E. coli* (Novagen, Madison, WI) and grown overnight in LB broth with kanamycin (30 µg/ml) and chloramphenicol (34 µg/ml). This culture (12 ml) was used to inoculate 500 ml 2XYT with the same antibiotics and the culture was induced with IPTG at an OD₅₆₀ of 0.44 to a final concentration of 1.2 mM. Four hours post-induction, the bacteria were harvested and sonicated in 20 mM Tris (8.0), 100 mM NaCl, 0.1% DOC, 20 µg/ml Leupeptin, 20 mM PMSF followed by centrifugation at 26,000 X g. The resulting pellet was resuspended in 8 M urea, 20 mM Tris (8.0), 100 mM NaCl and bound to Pro-bond nickel resin (Invitrogen, Carlsbad, CA). The column was washed several times with the above buffer then eluted with an imidazole gradient (50 mM, 100 mM, 500 mM imidazole was added to 8 M urea, 20 mM Tris (8.0), 100 mM NaCl). The eluates containing the protein of interest were then dialyzed against 10 mM Tris (8.0).

The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbRa3-38 kD-Tb38-1) are provided in SEQ ID NO: 152 and 153, respectively.

A fusion protein containing the two antigens TbH9 and Tb38-1 (hereinafter referred to as TbH9-Tb38-1) without a hinge sequence, was prepared using a similar procedure to that described above. The DNA sequence for the TbH9-Tb38-1 fusion protein is provided in SEQ ID NO: 156.

The ability of the fusion protein TbH9-Tb38-1 to induce T cell proliferation and IFN- γ production in PBMC preparations was examined using the protocol described above in Example 1. PBMC from three donors were employed: one who had been previously shown to respond to TbH9 but not Tb38-1 (donor 131); one who had been shown to respond to Tb38-1 but not TbH9 (donor 184); and one who had been shown to respond to both antigens (donor 201). The results of these studies (Figs. 5-7, respectively) demonstrate the functional activity of both the antigens in the fusion protein.

A fusion protein containing TbRa3, the antigen 38kD, Tb38-1 and DPEP was prepared as follows.

Each of the DNA constructs TbRa3, 38 kD and Tb38-1 were modified by PCR and cloned into vectors essentially as described above, with the primers PDM-69 (SEQ ID NO:150 and PDM-83 (SEQ ID NO: 205) being used for amplification of the Tb38-1A fragment. Tb38-1A differs from Tb38-1 by a *Dra*I site at the 3' end of the coding region that keeps the final amino acid intact while creating a blunt restriction site that is in frame. The TbRa3/38kD/Tb38-1A fusion was then transferred to pET28b using *Nde*I and *Eco*R1 sites.

DPEP DNA was used to perform PCR using the primers PDM-84 and PDM-85 (SEQ ID NO: 206 and 207, respectively) and 1 μ l DNA at 50 ng/ μ l. Denaturation at 94 °C was performed for 2 min, followed by 10 cycles of 96 °C for 15 sec, 68 °C for 15 sec and 72 °C for 1.5 min; 30 cycles of 96 °C for 15 sec, 64 °C for 15 sec and 72 °C for 1.5 min; and finally by 72 °C for 4 min. The DPEP PCR fragment was digested with *Eco*R1 and *Eco*T21 and clones directly into the pET28Ra3/38kD/38-1A construct which was digested with *Dra*I and *Eco*R1. The fusion construct was confirmed to be correct by DNA sequencing. Recombinant protein was prepared as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-2) are provided in SEQ ID NO: 208 and 209, respectively.

The reactivity of the fusion protein TbF-2 with sera from *M. tuberculosis*-infected patients was examined by ELISA using the protocol described above. The results of these studies (Table 11) demonstrate that all four antigens function independently in the fusion protein.

TABLE II
 REACTIVITY OF TbF-2 FUSION RECOMBINANT WITH TB AND NORMAL SERA

Serum ID	Status	TbF OD450	Status	TbF-2 OD450	Status	ELISA Reactivity			
						38 kD	TbRa3	Tb58-1	DPEP
B931-40	TB	0.57	+	0.321	-	-	-	-	+
B931-41	TB	0.601	-	0.396	-	-	+	+	-
B931-109	TB	0.484	-	0.404	-	-	+	+	-
B931-132	TB	1.502	-	1.292	-	-	+	+	-
5004	TB	1.806	+	1.666	-	-	-	-	+
15004	TB	2.362	-	2.468	-	+	+	+	-
39604	TB	2.443	-	1.722	-	-	+	+	-
08004	TB	2.871	-	2.575	-	-	-	-	-
96004	TB	0.691	-	0.971	-	-	-	-	-
107004	TB	0.875	-	0.732	-	-	-	-	-
92004	TB	1.632	-	1.304	-	-	-	-	-
97004	TB	1.491	-	1.979	+	+	+	+	-
118004	TB	3.182	+	3.045	+	+	+	+	-
173004	TB	3.644	-	3.378	-	-	+	+	-
175004	TB	3.332	-	2.916	-	-	-	+	-
274004	TB	3.696	-	3.716	-	-	-	-	-
276004	TB	3.245	-	2.56	-	-	-	-	-
282004	TB	1.249	-	1.234	-	-	-	-	-
289004	TB	1.273	-	1.17	-	-	-	-	-
308004	TB	2.708	-	3.355	-	-	-	-	-
314004	TB	1.663	-	1.398	-	-	-	-	-
317004	TB	1.163	-	0.92	-	-	-	-	-
312004	TB	1.709	-	1.453	-	-	-	-	-
380004	TB	0.228	-	0.461	-	-	-	-	-
451004	TB	0.18	-	0.2	-	-	-	-	-
478004	TB	0.188	-	0.469	-	-	-	-	-
410004	TB	0.384	-	2.392	-	-	-	-	-
411004	TB	0.306	-	0.874	-	-	-	-	-
421004	TB	0.337	-	1.456	-	-	-	-	-
528004	TB	0.047	-	0.196	-	-	-	-	-
A6-87	Normal	0.094	-	0.063	-	-	-	-	-
A6-88	Normal	0.214	-	0.19	-	-	-	-	-
A6-89	Normal	0.248	-	0.125	-	-	-	-	-
A6-90	Normal	0.179	-	0.206	-	-	-	-	-
A6-91	Normal	0.135	-	0.151	-	-	-	-	-
A6-92	Normal	0.064	-	0.097	-	-	-	-	-
A6-93	Normal	0.072	-	0.098	-	-	-	-	-
A6-94	Normal	0.072	-	0.064	-	-	-	-	-
A6-95	Normal	0.125	-	0.159	-	-	-	-	-
A6-96	Normal	0.121	-	0.12	-	-	-	-	-
Cut-off		0.284		0.266					

A fusion protein containing TbRa3, the antigen 38kD, Tb38-1 and TbH4 was prepared as follows.

Genomic *M. tuberculosis* DNA was used to PCR full-length TbH4 (FL TbH4) with the primers PDM-157 and PDM-160 (SEQ ID NO: 348 and 349, respectively) and 2 μ l DNA at 100 ng/ μ l. Denaturation at 96 °C was performed for 2 min, followed by 40 cycles of 96 °C for 30 sec, 61 °C for 20 sec and 72 °C for 5 min, and finally by annealing at 72 °C for 10 min. The FL TbH4 PCR fragment was digested with EcoRI and Sca I (New England Biolabs) and cloned directly into the pET28Ra3/38kD/38-1A construct described above which was digested with DraI and EcoRI. The fusion construct was confirmed to be correct by DNA sequencing. Recombinant protein was prepared as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-6) are provided in SEQ ID NO: 350 and 351, respectively.

A fusion protein containing the antigen 38kD and DPEP separated by a linker was prepared as follows.

38 kD DNA was used to perform PCR using the primers PDM-176 and PDM-175 (SEQ ID NO: 352 and 353, respectively), and 1 μ l PET28Ra3/38kD/38-1/Ra2A-12 DNA at 110 ng/ μ l. Denaturation at 96 °C was performed for 2 min, followed by 40 cycles of 96 °C for 30 sec, 71 °C for 15 sec and 72 °C for 5 min and 40 sec, and finally by annealing at 72 °C for 4 min. The two sets of primers PDM-171, PDM-172, and PDM-173, PDM-174 were annealed by heating to 95 °C for 2 min and then ramping down to 25 °C slowly at 0.1 °C/sec. DPEP DNA was used to perform PCR as described above. The 38 kD fragment was digested with Eco RI (New England Biolabs) and cloned into a modified pT7 Δ L2 vector which was cut with Eco 72 I (Promega) and Eco RI. The modified pT7 Δ L2 construct was designed to have a MGHHHHHH amino acid coding region in frame just 5' of the Eco 72 I site. The construct was digested with Kpn 2I (Gibco, BRL) and Pst I (New England Biolabs) and the annealed sets of phosphorylated primers (PDM-171, PDM-172 and PDM-173, PDM-174) were cloned in. The DPEP PCR fragment was digested with Eco RI and Eco 72 I and cloned into this second construct which was digested with Eco 47 III (New England Biolabs) and Eco RI. Ligations were done with a ligation kit from Panvera (Madison, WI). The resulting construct was digested with NdeI (New England Biolabs) and Eco RI, and transferred to a

modified pET28 vector. The fusion construct was confirmed to be correct by DNA sequencing.

Recombinant protein was prepared essentially as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-8) are provided in SEQ ID NO: 334 and 355, respectively.

One of skill in the art will appreciate that the order of the individual antigens within the fusion protein may be changed and that comparable activity would be expected provided each of the epitopes is still functionally available. In addition, truncated forms of the proteins containing active epitopes may be used in the construction of fusion proteins.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

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 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
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 - (A) APPLICATION NUMBER:
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(2) INFORMATION FOR SEQ ID NO:1:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGGACCGG	GTAGTTTGAA	CCAAACGCAC	AATCGACGGG	CAACGGAACG	GAAGAACACA	60
ACCATGAAGA	TGGTGAATTC	GATCGCGCGA	GGTCTGACCG	CGCGCGCTGC	AATCGCGCGC	120
GCTCGCGCGG	GTGTGACTTC	GATCATGGCT	GGCGCGCGGG	TGCTATACCA	GATGACGCGC	180
GTCTCTTTG	CGCGCGCACT	GGCTTGGAC	CGCGCATCCG	CGCTGACCT	CGCGACCGCC	240
GGCAGTTGA	CCAGCGCTGT	CAACAGCGTC	GGCGATCCCA	ACGCTGCTGT	TGCGAACCAAG	300
GGCAGCTGCG	TCGAGGGCGG	CATCGGGGGG	ACCGAGCGCG	GCATCGCGCA	CCACAGCTG	360
AAGAAGGCGG	CCGAGCAGCG	GGATCTGGCG	CTGTCTCTCA	GGTGACGAA	CATCGAGCGC	420
CGCGCGCGCG	GTTCGGCCAC	CGCGCACTT	TCCCTCTCGG	GTCCGAAGCT	CTGTGCGCGG	480
GTACCGCAGA	ACGTCACTTT	CTGGAATCAA	GGCGGCTGGA	TGCTGTCAAG	CGCATCGCGG	540
ATGGAAGTTC	TGCAGGCGCG	AGGGAACCTG	ATTGCGCGCG	CGGTTTCAG	CGCTGTCTCA	600
GCTACGCGCG	CGCGCTGGTG	ACGCGTCCAT	GTGGAACACT	CGCGCTGTGA	GCACGGTGGG	660
GTCTCGCGAG	GGGCGCAGCG	ACCGCGCGGT	GCAAGCGCTC	CTCGAGATAG	GTGGTGTCTC	720
GACACGAGAG	ANACCGCCCN	NNTCGNCTNT	TCTCGTNTNT	GNATGA		766

(2) INFORMATION FOR SEQ ID NO:1:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 762 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCATCACC	ATCACCATCA	CGATGAAGTC	ACGGTAGAGA	CGACCTCGGT	CTTCGCGCGA	60
GACTTCTCTA	GCGAGCTCGA	CGCTCTCTCG	CAAGCGGGTA	CGGAGAGCGC	GGTCTCGGGG	120
GTGGAAGGGG	TCCCGCGGGG	CTCGCGCTTG	CTGGTAGTCA	AACGAGGCGC	CAACCGCGGG	180
TCCCGGTTTC	TACTCGACCA	AGCCATCAGC	TCGGCTGGTC	GGCATCCCGA	CAGCGACATA	240
TTCTCGAGC	ACGTGACCTT	GAGCTGTCTG	CATGCTGAAT	TCCGCTTGGG	AACACAGCAA	300
TGCAATGTCC	TCGATGTCCG	GAGTCTCAAC	GGCAGCTAGC	TCAACCGCGA	GGCCGTGGAT	360
TCGCGCTGTC	TGGCGAAGCG	CGACGAGGTC	CAGATCGGCA	AGCTCGCGTT	GGTCTCTTTC	420
ACCGAGCCCA	AGCAAGCGCA	GGATGACCGG	AGTACCGGGG	GGCCGTGAGC	GCACCCGATA	480
GGCCCGCGCT	GGCGGGGATG	TGATGCGGGG	CGGTCTCTCG	ACCTGCTACG	ACCGGATTTT	540
CGCTGATGTC	CACCATCTTC	AAGATTGGAT	TCTTGGGAGG	CTTGAGGGTC	GGGGTGACCT	600
CCCGCGCGCG	CTCATCTGGG	GGTTCGCGCN	GGTTCTCACCG	CNTACGCACT	GGCNCCTGGN	660
TTCNAATTC	NTTCTTCTCT	GGCCGGAAGG	GGACNTTAN	CTTGCGCGCTN	GAAGAGGTGA	720
TCGCGGGCCC	NTCTTGGAAN	CCGCTTCCCC	CT			762

(2) INFORMATION FOR SEQ ID NO:2:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 813 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATATGCATC	ACCATCACCA	TCACACTTCT	AACCGCGCAG	CGCTCGGGG	GGCTCGAGCA	60
CCACGCGACA	CGGGCGCGCA	TGATCTGCT	AGCTTGAGTC	TGGTCAGGCA	TGCTGTCGAG	120
CAGCGCGATG	CCCTATTTT	GTCTCGACT	CAGATATCGC	GGCATCCAA	TCTCCGCGCT	180

CGCGCGCGCG	GTGCTGCAAA	CTACTCCGGG	AGGAATTTGG	ACGTGCGCAT	CAAGATCTTC	240
ATGCTGGTCA	CGGCTGTCT	TTTCTCTGT	TGTTGGGGTG	TGGCCACGGC	CGGCGCCNAG	300
ACCTACTGG	AGGAGTTGAA	AGGCACCGAT	ACCGGCGAGG	CGTGCCAGAT	TCAAAATGTC	360
GACCCGGGCT	ACAACATCAA	CATCAGGCTG	CCCAATTAAT	ACCGCGACCA	GAATTCGCTG	420
GAATAATTACA	TGCGCCAGAG	CGCGGACCAAG	TTCTTCAGCG	CGGCGACATC	GTCCATCTCA	480
CGCGAAGCCC	CCTACGAATT	GAATATCACC	TGCGCCACAT	ACCAATCCGC	GATACCGCGG	540
CCTGTACGC	AGGCGGTGGT	GCTCAGGCTC	TACCAACAAG	CGGCGGCGAC	GCACCCCAAG	600
ACCACTACG	AGGCGGTGGA	TTGGGACCGG	CGCTATCGCA	AGCCAATCAG	CTATGACAACT	660
CTGTGGCAGG	CTGACACCGA	TCCGCTGCCA	GTCTCTCTTC	CCATTGTTCG	AAGGTGAAGT	720
GAGCAACGCA	GACCGGAGCA	ACNGGTATCG	ATAGCCCGCN	AATGCCGGCT	TGGAACCCNG	780
TGAATTTATC	ACAACCTTGC	AGTCACNAAA	NAA			813

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTATGAAC	ACGCGCGGCT	CGGATAACTT	CCAGCTGTCC	CAGGGTGGGG	AGGGATTGCG	60
CATTCCGATC	GGGACGGCGA	TGGCGATCGC	GGGCCAGATC	CGATCGGGTG	GCGGCTGACC	120
CACGGTTCAT	ATCGGGCGTA	CGGCTTCTCT	CGGCTTGGGT	GTGTGTCACR	ACAACGGCGAA	180
CGGCGACGCA	GTCCACCGCG	TGGTCGGGAG	CGCTCGGGCG	GCAAGTCTCG	GCATCTGAC	240
CGGCGACGCG	ATCACCGCGG	TGGACGGCGC	TCCGATCAAC	TGGGCCACCG	CGATGCGCGA	300
CGGCGATTAAC	GGGATCATC	CGGCTGACGT	CATCTCGGTG	AAGTGGCAAA	CGAAGTGGGG	360
CGGCGACCGT	ACAGGGAACG	TGACATTCGC	CGAGGACACC	CGGCGCTGAT	TTCGTCGGGG	420
ATACGACCG	CGGCGGGGCC	AATTGGA				447

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCCATCTC	GCTCGCGGAG	TATGTGCGCC	AGCAATATGC	TGGCAGCTGC	CTAACGGAAT	60
CGGCTGATCC	GACGTGCGAG	GTGTGGAAC	CGGCGCGCGC	GGAGATATCG	GTCCATGCTCT	120
AGGCTCGGCG	CGGCGAGCTC	CGGAATGGCG	CGAGTGAGGA	GGCGGGCAAT	TTGGCGGGCG	180
CGGCGGACGG	GGAGCGCGCG	AATGCGCGCA	GTGAGGAGGT	GGCACTGAT	GCCCGAGGTG	240
ATCCAAATCA	CCTGATTTGC	GNGTNGNGGN	CGATTTGACA	ATCGAGGTAG	TGACCGCAAA	300
TGAATTAATG	AAAACGGGNG	GNGAGCTCGG	NTGTTCTGGT	GGTGNTAGGT	GNGTNGCTGG	360
NGTNGNGGNT	ATCAGATGAT	TCTTCGNGCA	AAATGATGNG	CGAGGAACAG	GGTGTGCGCG	420
NNANNCCNAN	GNGTCCNAN	CCNNNNNTCC	TGNGCGANAT	CANAMAGNGC	NTTATGNGGA	480
NAAAGCGGTG	GANCAGNNNN	AANTNGNGNG	CCHAAMAAAC	NNNANNNGNG	NNAGNTNGNT	540
NNNTNTTNC	NNNNNNNTNG	NNNNNNNNCN	NNNLANCNCN	NTNNNNNGAA	NNGGNTTNTT	600
NAAAT						604

(2) INFORMATION FOR SEQ ID NO:6:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGCAGTCTG	AACCACTTCA	CTAAAGGGAA	CAAAAGCTTG	AGCTCCACGG	CGGTGGCGGC	60
CGCTGTAGAA	CTAGTGKATM	YYTGGGCTG	CAGGAATYCG	GYACGAGCAT	TAGGACAGTC	120
TAACGGTCTCT	GTTACGGTGA	TGGAATGACC	GACGACATCC	TGCTGATCGA	CACCGACGAA	180
CGGGTCCGAA	CCCTCACCCT	CAACCGGCGG	CAGTCCGGYA	ACGGCTCTTC	GGCGGGCTTA	240
CGGGATCGGT	TTTTCGGGGY	GTGGGTCGAC	GGCGAGGYCG	ACGACGACAT	CGAGCTCTTC	300
ATCTTCACCG	GYCGCGATCC	GGTGTCTGCG	GGCGGACTCG	ACCTCAGAGT	AGCTGGCGCG	360
GCAGACCGCG	GTGCGCGACA	TCTCACCGCG	GTGGCGGGCC	ATGACCAAGC	CGGTGATCGG	420
CGCGATCAAC	GGCGCGCGCG	TGACCGCGCG	GCTCGAAGTG	GGCTGTACT	GGGACATCTT	480
GATGGCTTTC	GAGCAAGGCC	GCTTCGCGGA	CACCGACGCC	CGGTGGGGCG	TGCTGCCAC	540
CTGGGACTTC	AGTGTGTGGT	TGCGGCAAAA	GCTGGGATC	GGCTGGGGCG	GGTGTATGAG	600
CGTACCGCGG	GACTACCTGT	CGTGAACGGA	CGC			632

(2) INFORMATION FOR SEQ ID NO:7:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACGAGGAC	GGCGCGCGAG	AGCGGGCGCG	AACGGCGGATC	GACGCGCGCC	TGGCGAGAT	60
CGGCACTCAC	CAGGAGGGAG	TGGAATCATG	AAATTGTCTA	ACCATATTGA	CGCGCTCGCG	120
CGCGCGCGAG	CGCGCGCGCG	GGTGGCGGAG	GTCTATGCGG	AGGGCGCGCG	CGAGTTTCGGC	180
CGGCTGCGCG	AGCGCGCTCG	CATGCTGTCC	CGGACGAGGG	GACTGTCTAC	CGCGGGCTGCG	240
CGGACGTTTC	CGGAGACACT	GCTGGTGGCG	CAGGTGGCGC	GTGGCTCGAA	GGAGCGGGTC	300
CGCGCGCGCG	TGCGCGCGAG	CTGCGCTGCG	CGCTGTGTGG	TGAGCGCACG	CACCAACATG	360
CTGTACGCGG	CAGCGCAAAAC	CGGACCTGCG	CGGCGCATCT	TGGCGGGCGC	AGCAGCTGCG	420
CGCGGTGAGC	CGAACCGCGC	GTATGTGGCG	TGGCGGGCGC	GAACCGGGAG	ACCGCGGGGA	480
CGCGCGCGAC	CGTTTCGGCG	GGATGTGCGC	GGCGAATACC	TGGCGCACCG	GGTGAATTC	540
CACCTCATCG	CAGCGCTGGT	CTGGTGTGCG	CTGGACRAAA	CGTTCTGCGG	GGGGGGCGCG	600
CGCGCGCGAC	AGCTCATGCG	CGCGCGCGGT	GGATGTGTGT	TGCGCGCGCA	GGTGGCGCGC	660
GAGCATCGCG	CGCGCGCGCT	CACCGCGCGG	CTCGAGCTCG	GAACCGCGCG	CGGCGATCTG	720
GCATGGGCGA	CACCGTTCGA	GGCATATGCA	AGCGGCTTTC	CGCGGCTCGG	CGACCACTTC	780
TGGCAGCGCG	AGCGAATGCC	GATGAGCACT	CGTCAAGTGG	TCAGGCGGGT	CGTGGGCTCG	840
CGCGCGGACC	TGACCGCGCG	CACCGTCTCT	CGCTGAGCGA	ACGAGCACAC	CGCGGAGCTG	900
GTGACCGAGC	ACGAGCTGCG	CGCGCGCGGA	TGCTGTCTCG	ACACCGATGC	GGGCTGTGTT	960
GGCGCGCTGG	CTTGGGCGCG	CTTCACCGCG	GGCGGCGCA	TCGGCACCTG	GATCGGGCGC	1020
CGCGCGGAGG	GGCAGGTGTC	GGCGGAAAC	CGGACTGGGT	GAGTGTGCGC	GGCTGTGCGG	1080
TAGGTTGTCA	TGCGTGGCGC	GAGGATCTTC	CGCGGCGCGA	ACGGAGGTGG	CGACACAGGT	1140
GGAGCTCGCG	CGCACTGGCT	TGCGCGCGAA	CGCGTCTGTT	GGCGTGGGTT	TGGCGCGACT	1200
GGCGGATCGC	GTGGCGCGCG	GGCTTGGCG	GAGGCTCGAG	CTCAACGTGC	CGTACCGGAA	1260
GGACCGGAGC	GTACCGCGGG	GTACCTGTCG	GGCGCGAAGG	AA		1320

(2) INFORMATION FOR SEQ ID NO:8:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGACGACCC	CGATATGCGG	GSCACCCUAG	CGAAGCCUAT	CGCGGACGCA	CTCGGGCGCG	60
TGATCGCTCC	CGTTGAGGAC	ATTGAGGACT	CGCTGGAGGC	CGGCTGGGG	GAGCGCGGTC	120
GTATGACCT	GGCCCGTGT	TACATCATCT	ACCGGACGG	GGCGCGGAG	CTGCGGACCG	180
CTAAGGCTT	GCTCGGCTG	CGGACGAGT	TAAAGCTGAG	CTTGGCGGCC	GTGACGGTAC	240
TGCGCGAGCG	CTATCTGCTG	CAGGACGAGC	AGGGCGCGCC	GGCGGAGTGG	ACCGCGGAGC	300
TGATGAGCG	ATCGCGCGCC	TGTGTGCGCG	CGGCGGAGGA	CGAGTATGAG	CGGCGCTCGT	360
CGAGCGGCTG	GGCGGACCG	TTGCGCAGCC	TATTACGCAA	CGTGGGAATC	CTGCGGAATC	420
CGCCCACTTT	GATGAATCT	GGCAGCGACC	TGGGACTGCT	CGCGGCTGCT	TTGTGTCGCG	480
CGATTGAGGA	TTGCTGCAA	TGGAATCTTG	CGAGCGTGGG	ACAGGCGCGC	GAGCTGCAAG	540
GGGCTGGAGG	CGGACCGGA	TATGCTTCA	GGCAGCTGCG	ACCGCGCGGG	GATCGGGTGG	600
GCTTCACGGG	GGGACCGGC	AGCGGACCGG	TGTCGTTCT	ACGGCTGTAT	GACAGTCCCG	660
CGGGTGTGCT	CTGCTGGCT	GCTCGCGCGG	GTGCGGCTG	TATGGCTGTG	CTTGATGTGT	720
CGGACCGGA	TATCTGTGAT	TTGCTCACCG	CGAAGCGCGA	ATCGCGGAGC	GAGCTCCCGC	780
ATTTCACCT	ATCGGTGGT	GTGACCGAGC	CGTTCCTGCG	GGCGCTCGAA	CGCAACGGGC	840
TACACCGGCT	GATCAATCG	CGAACCGGCA	AGATGCTGCG	CGCGATGCGC	GGCGCGGAGC	900
TGTTGACGCG	CACTGCGAA	GGCGCGCAGC	CGGCTGGCGA	TCCCGGGCTG	GTGTTCTCG	960
ACAGCATCAA	TAGGCGAAG	CGGCTGGCGG	GGGAGGCGCG	CGATGAGGCG	ACCAACCGCT	1020
CGGGGAGGCT	CGGCTGCTG	CGTTACGAGT	CAGTAACTCT	CGGCTGGATC	AACCTCGGCG	1080
GATGCTGCG	CGACGCTGCG	GTGAGCTGGG	ACCGGCTCGA	GGAGGTGCGC	CTCATGCGTC	1140
CGGCGCTGCT	TGATGAGCTC	ATCGATGCTA	GGCGCTACCC	CTTCCCGGAA	CTGGGTGAGG	1200
CGGCGCGCGC	CAGCGCGAAG	ATCGGCTGCG	GAGTATGCG	TTTGGCGGAA	CTGCTTTGCG	1260
CAGTGGGTAT	TCCGTACGAC	AGTGAAGAAG	CGGTGCGGTT	AGCCACCTCG	CTCATGCGTC	1320
GGCATACGCA	GGCGGCGCAC	ACGGCATCGC	GGAGGCTGCG	CGAAGAGCGG	GGGCGATTCT	1380
GGCGCTTCC	CGATAGCGCG	TTGCGCGGCT	CGGGCGCGAG	CGGCAACGCA	CAGGTGACCT	1440
CTGCTGCTCC	GACGGGCA					1458

(2) INFORMATION FOR SEQ ID NO:9:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 562 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGGTGTGAT	GTGCTGGAT	CTGGAACCCG	GTGGCCCGCT	ACCTACCGAG	ATCTACTGCG	60
GGCGCAGGGG	GTGCGCTG	GGCATGCGGG	TGCTGTGAGT	CGGATGCGCG	GTGCGCATCG	120
TGATGCTGTT	GTGACGAGC	AGCGCGGCTG	CGAAACCGGT	CAGCGCGGAC	AAGCGCGGCT	180
CGCGCCAGAG	CGATCGGGC	TGCGCGGCAC	CGCAAGCACC	CGAGCGGGCC	GGGCAAACTG	240
AAGGTAACTG	CGCGCGGGC	CGGCGCGAGG	GGCAAAACCG	CGAGACACCT	ACGCGCACCG	300
CGCGGTGCA	CGCGCGGCG	GTGCTCAAGG	AAGGGGACGA	TGCTGCGGAT	TGACGCTCGG	360
CGGTCAAAGG	TTTGACCAAC	GGCGCGGAGT	ACTACGTGCG	CGACCAAGCG	AGATTACCA	420
TGTTGTGAC	CGACATGCGC	CTGGTGTGCT	GTAAACGCGA	CGTTGGGGCG	GGGTTGTTGG	480
CGGCTTACGT	TACTGCTG	GACAACAGCG	GGTGTGTGTC	CAGCTTGGAC	TGCGCGCTCT	540
CGAATGAGAC	GCTGTGCAAG	ACGTTTTTCC	CGGTTGAGCA	GCTAACGACC	CGCGTGACCT	600

GGACCGGAT	GGGATCGGCG	CGCGCTGCG	CATTGCGCG	GCGCGGATC	GGCGCGGCA	669
CCTACAACT	CGTGGTACAA	CTGGGCAATC	TGCGCTCGCT	GCGGCTCGCG	TTCACTCTGA	720
ATCAGCGCG	GCGCGCGCG	GCGCGCGTAC	CGCTCGCGG	TCCAGCGCG	GCGCGCTCG	780
CGGAGTCTC	CGCGCAAGCG	GGATAATTAT	TGATCGCTGA	TGGTGGATTG	CGCGCGGCT	840
GACACCCCT	CGCTCGTGC	CG				862

(2) INFORMATION FOR SEQ ID NO:10:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 622 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGATGACGA	CGCGCAAGCG	GTGACATGCC	TCCCTGGGTC	TGCAGGTGAC	CAATGACAAA	50
GACACCCCG	GCGCCAAGAT	CTGGAAGTA	GTGGCTGGTG	GTGCTGCGC	GAACGCTGGA	120
GTGCGGAAG	GCGCTGTTGT	CACCAAGGTC	GACGACCGCC	CGATCAACAG	CGCGGACCG	180
TTGGTTGCG	CGTGGCGGTC	CAAGCGCGCG	GCGCGCACGG	TGGCGCTAAC	CTTTGAGGAT	240
CCCTCGGCG	GTAGCGCGAC	AGTGCAAGTC	ACCTCTGGCA	AGCGCGAGCA	GTGATCAAGG	300
TGCGCGCGCA	GTGTTCAAA	CTCGATATA	CGTGGGACG	CATGGAACAG	CGTTCGAGT	360
TGGTGGTGG	CGCGGCACTT	GTGCTGTGTC	TTGACGATCG	CACGCGCGAC	GGCGATGAAG	420
ACGACAGCG	GCGCTGTGTC	ACCGAGTGG	TGACCGAGCG	CGGTTTGT	GTGACGCGCG	480
TGCTGGCGT	GTGCGCGGAC	GAGGTGAGCA	TCCGAAATGC	GCTGAACACA	GCGGTGATCG	540
CGGGGTTGA	CGTGTGGTGG	TGCTGCGCG	GGACCGGCT	GACGCTGCG	GATGTCACCG	600
CGGAAGCCAC	CCGAGACATT	CT				622

(2) INFORMATION FOR SEQ ID NO:11:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCGAGCGG	TAAGCCTTT	GGCGCGCGCG	ACACTGGTGT	TGACAGCATG	CGCGGCTGCG	60
ACCAACAGCT	CGTCTGCTAG	CGCAGCGCGA	ACGTCGCGGT	CGGTGCACTG	CGCGCGCAAG	120
AGAGAGCTTC	ACTCCAGCGG	CTGACCGGCA	CAAGAAAATG	CGATGGAGCA	CTTCTGTAT	180
GCTTACGTGC	GATCTGTGCG	GGCTACAGCG	TTGCACTACA	ACGCCAACGG	GTCCGCTGCG	240
GGGTGAGCG	AGTTTCTCAA	CAACGAAACC	GATTTCGCGG	GCTCGGATGT	CGCGTTGAAT	300
CGCTGAGCG	GTCAAGCTGA	CGGCTCGCGG	GAGCGGTGCG	GTTCGCGCGG	ATGGGACCTG	360
CGGACGCTGT	TGCGGCGGAT	CGGATCAGCT	TACATATCA	AGGGCGTGAG	CACGCTGAAT	420
CTTGACGCG	CGACTAACCG	CAAGATTTC	AACGGGACCA	TCACCGTGTG	GAATGATCCA	480
CAGATCCAG	CGCTCAACTG	CGGCAACGAC	CTGCGCGCAA	CACCGATTAG	CGTTATCTTC	540
CGGAGCGACA	AGTCCGCTAC	CTGCGACAA	TTCCAGAAAT	ACCTCGACGG	TGTATCCAA	600
GGGGGCTGG	GCAAGGCGCG	CAGCGAAACG	TTGACGCGGG	GCTCGGCGGT	CGGCGCGCAG	660
GGGAACACG	GAACGTGCGG	CGTACTGCG	ACGACCGAGG	GCTCGATCAC	CTACAACGAG	720
TGCTGCTTG	CGGTGGGTAA	GCACTTGAAC	ATGGCGCGAG	TGATCACGTC	GCGCGGTGCG	780
GATCAGTGG	CGATGCCAC	CGAGTGGGTC	GCTAAGACAA	TGCGCGGGCG	CAAGATCATG	840
CGACAAGCG	ACGACTGTGT	ATTGACACG	TGCTGCTGCT	ACAGACCGAC	CCAGCTTGGC	900
TCTTACGGA	TGCTGTGCG	GACCTATGAG	ATGCTGCTGT	CGAATATGCG	GGATGCGAGC	960
ACCGTACTG	CGGTAAAGCG	GTCTATGCAA	GCGCGGATTC	GTCCAGGCGCA	AGAAAGCCTG	1020

GAGCAATACG	GCTCCATTCC	GTTCGCCAAA	TGTTTCCAAG	CAAAATTGGC	GGCCGCGGTG	1080
AATGCTATT	CTTGACCTAG	TGAAGGGAA	TCGACGGTGA	GGGATGCCGT	TCGCGCAGTA	1140
GGGTGCGAAT	TTGGGCGGTA	TCAGCTATTG	CGGCTGCTGG	GGCGAGGGCG	GATGGGCGAG	1200

(2) INFORMATION FOR SEQ ID NO:12:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1188 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAAGCAGCT	GCAGGTGCTG	CTGTTCGACG	AACGGGCGAT	GGCGAAGACC	AAACGCACCA	60
AGACGGGCTA	CACGACGAGT	GGCGACGCGC	TGCAGTCGTT	GTTCGACAAAG	ACCGGGGCATC	120
CGTTTCTGGA	ACATCTGCTC	GGCCACGCGG	ACGTCACGCG	GCTCAAGGTC	ACCGTCGACG	180
GGTTCTCGCA	AGCGGTGGCC	GGCGACTGCG	GCATCGACAC	CACGCTCAAC	CAGACGATCG	240
GGCGACGCGG	CGGGTCTGCG	TGCACTGAAAC	CCAACCTGCA	GAACATCCCG	ATCCGACACG	300
ACCGCGGCGG	GGGATCCGCG	GACGCTTTCG	TGTCGCGGGA	CGGTTACGCT	GAGTTGATGA	360
CGGCGGACTA	CAGCGAGATC	GAGATGCGGA	TCATGGGGCA	CGTGTCTGGG	GACGAGGGCC	420
TGATCGAGGC	GTTCACACCC	GGCGAGGACC	TGTTATTCGT	CGTGCCTGCG	GGGTTGTTCC	480
GTGTGCCCAT	CGACGAGGTC	ACCGCGGAGT	TGCGCGGCGC	GTTCAGGCGG	ATGTCCTACG	540
GGCGGTTCTA	CGGTTGAGC	GGCTACGCGC	TGTCGACGCA	GTTCAGAAATC	TCCACCGAGG	600
AAACCGACCA	GCAGATGGAC	GGGTATTTCG	CGCGATTTCG	CGGGGTGCGC	GACTACCTGC	660
GGCGGTAGT	CGAGCGGGCC	CGCAGGACG	GCTACGCTTC	GAGCGTGGTG	GGCGGTCGCG	720
CGTACCTGCG	CGAGCTGGAC	AGCAGCGACC	GTCAAGTGGC	GGAGGCGCGC	GAGCGGGGCG	780
CGCTGAACGC	GGGATGCGG	GGCAGCGCGG	CGCACATCAT	CAAGGTGGCG	ATGATCCAGG	840
TGCGCAATGC	GGTCAACGAG	CGCACGCTGG	CGTTCGCGAT	GCTGCTGCGC	GTTCACGACG	900
AGATGCTGTT	CGAATCGCG	CGCGGTGAAC	GGCAGCGCGT	CGAGGCGCTG	GTGCGCGACA	960
AGATGGGCGG	CGCTTACCGG	CTCGACGCTC	CGCTGGAGGT	GTGCTGGGCT	TACGGGCGCA	1020
GTCTGGACGC	GGCGGCGCAC	TGAGTGCGCA	GGGTGCATCT	GGGCGGGGAA	TTGCGCGATT	1080
TTCTGCGCGT	GAGTTCAAGC	TCGGGCGCAT	CGGAGCGGAG	TTTGTCGACG	GTGTACCGCT	1140
CGAGTAGGCT	CGTCA					1185

(2) INFORMATION FOR SEQ ID NO:13:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCGCGCTC	TGCTGTTTGA	AGGGTTTTAC	CGGTGCGCAT	CGGCACGGGC	GTTCGCGGCT	60
TGCGCGCTCG	GCTTGGCGAT	CGTCAACAGC	GTGTTGCTCA	ACGACGCGCG	ATTGCTGCGC	120
ATCGAGAGCA	CGGACCGAGG	CGGCGAGCGC	CGTGAACGCT	CGATTATACG	GCTGCTGCGC	180
GGCGTTCGGA	TGCGGATTTG	CGAGCTTTCG	GGTGCACAGG	GTGGCGCTCG	GAGCAGCGGAC	240
ATCGAGAACT	CTCGGGGTTG	GGCGAACGTT	ATGTCAGTGG	AATCTCACTG	CACGCGCGCA	300
ACCTAGTTGT	GCAGTTACTG	TTGAAAGCCA	CACCATGGCC	AGTTCAGCGA	TGGCCAAAGTT	360
GGCGCGAGTA	GTGGGCTTAG	TACAGGAGAA	GCAACCTAGC	GACATGACGA	ATCAGCCACG	420
GTATTGCGCA	CGCGCGGAGC	AGCGCGGAAC	CGCAGCTTAT	GCTCAGGGGC	AGCAGCAAAAC	480
GTACAGCGCA	CAGTTCGACT	GGGCTTACCG	ACGTTCCCGG	CGCGCGGCGC	CAACCCAGTA	540
CGCTCAACCG	TACGAGGCGT	TGGTGTGTAC	CGGCGCGGCT	GTGATACGCG	GCGTGTATCG	600

GACCATGAGC	CCCCCTCTG	GGATGGTTGG	CGAACGCCCT	CGTGCAGGCA	TGTTGGCCAT	560
CGGCGGGGTG	ACGATAGGCG	TGGTGTCTGG	CGGCATCGGC	GGCGCGGGCG	CATCCCTGGT	726
CGGGTTCAAC	CGGCGACCGG	CCGCCCCGAG	CGGCGGGCCA	GTGGCTGCCA	CGCGCGCGCG	780
AAGCATCCCC	CGACCAAAAC	TGCGCGCGGG	GTGGGTGAA	CAGGTGGCGG	CGAACGTGGT	840
CGCCAGTGTG	GTCTGTTTGG	AAACCGATCT	GGCGCGCGAG	TGGGAGGAGG	GCTCCGCGAT	900
CATTCTGTCT	CGCGAGGGGG	TGACTTTGAC	CAACAACAC	GTGATCGCGG	CGGCGCGCAA	960
GCCCTCCCTG	GGCAGTCTCG	CGCGCAAAAC	GACGTAAC	TTCTCTGAGC	GGCGGACCGC	1020
ACCCCTCACG	GTGGTGGGGG	CTGACCCAC	CAGTGATATC	GCCGTCTGTC	GTGTTTCAGG	1080
CGTCTCCGGG	CTCACGCCGA	TCTCCCTGGG	TTCTCTCTCG	GACCTGAGGG	TGGGTCAAGC	1140
GGTGTGGGG	ATCGGGTCCG	CGCTCGGTTT	GGAGGGCAC	GTGACCAACG	GGATCGTCAG	1200
CGCTCTCAAC	CGTCCAGTGT	CGACGACCGG	CGAGGCCGGG	AACCAAGAAC	CGGTCTGGA	1260
CGCCATTGAG	ACCGAGCGCG	CGATCAACCC	CGGTAACTCC	GGGGCGCGCG	ACTCAGCCCA	1320
TGGCGAGAGC	GGCTCGATCG	GTCTCGGTTT	CATTGCCACG	CTGGCGCGCG	ACTCAGCCCA	1380
CGCGGACGAG	TTGATCAGCA	CGGCGAGGCG	GTGATTCCA	GTGACCCAGG	CGGTGAACTAT	1440
CAATGACMAA	GACACGCCCG	CGGCGAAGAT	GTGACATGCC	TGCTTGGGTG	GTGCTGTGAC	1500
GAAAGCTGGA	GTGCGCAAGG	CGCTCGTGTG	CGTCAAGTGA	GTGGCGCGGTG	GTGCTGTGCG	1560
CGCGGACCGG	TTGGTGGGGG	CGGTGGGGTC	CAAGCGCGTC	GGCGCGCGCG	CGATCAGACG	1620
CTTTCAGGAT	CGCTCGCGCG	GTGCGCGCAC	AGTGCAGTGC	ACCTCGCGCA	AGGCGGAGCA	1680
GTGATGAAGG	TGCGCGCGCA	GTGTTCAAGG	C			1740
						1771

(2) INFORMATION FOR SEQ ID NO:14:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1958 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(4) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTGCACCGCG	GTGGCGGGCG	CTCTAGAACT	AGTGGATCCG	CGGGGCTGCA	GGAAATTCGG	60
ACGAGGATCC	GACGTCGCAG	GTGTTGGAAC	CGCGCGCGCG	GGAAGTATCG	GTCCATGCTT	120
AGCCCCGGGA	CGGCGAGCGC	CGGAATGCGG	CGAGTGAGGA	GGCGGGCAAT	TTGGCGGGCG	180
CGGCGAGCGG	CGAGCGCGCG	AATGGCGCGA	GTGAGGAGCG	GGGCACTCAT	GCCCGAGGTG	240
ATCCAAATCA	CGTGCATTGG	GCTTGGCGCG	CGATTGACCA	ATCGAGGTAG	TGAGCGCAAA	300
TGAATGATCG	AAAACGCGCG	GTGAGGTCG	CTGTTCTGGT	GGTGTAGGTT	GCTTCCCTCG	360
CTGTGTGGCT	ATCGAGGATG	TCTTGGCGCA	AACCTGATGC	CGAGGAACAG	GGTGTTCGCG	420
GAGACCGGAC	GGCGTCCGAC	CGCGGCTCCG	TGCGCGGATG	CAGGCAAGTC	CTGTATCCGA	480
CAGAGGGGTT	GACCGAGGTG	CACGTAGCGG	TCCGAACAC	CGGGAAGTGC	GACAGCTTGC	540
TGGGTATTAC	CAGTGCAGAT	GTGCAAGTCC	GGGCGCAATC	GCTCGCGCGCA	AGGCGGATAT	600
GCACCTACAA	CGACGAGCAG	GGTGTCCCGT	TTGCGGTACA	AGGCGACAAAC	ATCTCGGTGA	660
AGCTGTTGGA	CGACTGGAGC	AATCTCGGCT	CGATTCTGTA	ACTGTCAACT	TCACGCGGTG	720
TGCAATCTCG	CGCTGGGGTG	ACGCGAGTGC	TGTTCGGGTG	CACGCAACCTC	CAAGCGCAAG	780
GTGCGGAAGT	GATAGAGCGA	ATTTCGACCA	CGAAATCAAC	CGGGAACATC	CGCGCGAGCT	840
GTGTCAGAGT	GCTTATCTCT	GGCGCCAGGA	GTGCAAGGCC	GGCGACCGTG	TGGATTGCCG	900
AGGACCGGCTC	GCACGAGCTC	GTGCGAGCGA	GCATCGAGCT	CGGATCGCGG	TGATTTCAAC	960
TCACGCACTG	GAAATGGAAC	GAACCGGCTC	AGGTGAGCTA	GGCGGAAGTT	CGGTGCAAGC	1020
GTGHTGGA	ACGCCCTTGT	GAAGGGTGTG	AACGGNAC			1058

(2) INFORMATION FOR SEQ ID NO:15:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 842 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA	CGAGAGGTGA	TGGACATCAT	CGGGACCAGC	CGACATCCT	GGGAACAGGC	60
GGCGGGGAG	GGGATCCAGC	GGGCGCGGGA	TAGCGTCCAT	GACATCCGG	TGCTCGGGT	120
CATTGAGAC	GACATGCGCG	TGGACAGCGC	CGCGAAGATC	ACCTACCGCA	TCAAGCTCGA	180
AGTGTGTTT	AAGATGAGGC	CGGCGCAAGC	GCCTTAGCAC	GGGCGGGGGA	GCAAGACGCA	240
AAATCGCACG	GTTTGCGGTT	GATTCGTGCG	ATTTTGTGTC	TGCTCGCGGA	GGCTTACGAC	300
GGCGGGGCCA	GGTCCGCGTG	CTGCGGTATC	CAGGCGTCCA	TGCGGATTC	GGCGGCCACG	360
CGGGAGTTAA	TGCTTCGCGT	CGACCGGAAC	TGGCGGATCC	GGCGGNGAGC	TGATCGATGA	420
CGGTGGCCAG	CGGTCGATG	CGCGAGTTGC	CGAGGGAAC	GTGCTCGGAC	GGCGGTAGGA	480
AGCGTCCGTA	GGGCGCGGTG	CTGACCGGCT	CTGCGTGGCG	CCTCAGTGGG	GGCAGCGAGC	540
GG						542

(2) INFORMATION FOR SEQ ID NO:16:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 913 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGTGCGGCG	CGCGCGTCCG	TTGCGCGCAT	TGCGCGGCTC	GGGATCAGC	TGCGCATCGC	60
CACCATCAGC	GGCTTTGCGC	CGGGCACCGC	CGGTGCGGCG	GGGCGCGGCG	ATGCCACGGC	120
TTGACGCTGG	CGCGCGGCGC	CGCATTTGCC	ATACAGCACC	CGGCGGGGCG	CACCGTTACC	180
GGCGTGGCGA	CGGTGCGGCG	CGCTGCGGTT	TGAGGCGGCG	GAGGCGGAAT	GAAAGCGGCG	240
CAAGCGCGCG	GGCGGACCGC	TTGCGCGGTT	TTGCGCGGCG	CGGCGCGGCG	CGGCGGAATTG	300
CGGAACAGCG	AMGACCGGTT	GGCGCGAGCG	CGGCGCGGCG	TACCGGCGCT	GGCGGCGGCG	360
GGCGCGGCGC	CGCGCATTAC	CGCGGTTGCC	GTTCGCTGCG	CGCGCGTTAC	CGGCGCGGCG	420
GTTCGCGGCG	AATATTGCGC	GGGACGCGCG	AGACCGCGCG	GGCGCACCAT	TGCGCGCGCG	480
CAGCGAAACA	ACAGCGCGAC	GGTCCGCGCG	GGCGCGCGCG	TTGCGCGCAT	CACCGCGCAT	540
TGACGCGCAG	CACCGCGGTT	AATGTTTATG	AACCGCGTAC	CGGCGAGCGG	GGCGGCGCAT	600
CGGCGCGGCG	GAGGCGGCGC	CGGCGCGGCG	CGGCGCGGCG	CGGCGCGGCG	GGGTTGCGAC	660
GGGCGCGGCG	GGAGCGGCGC	GTGCGCGGCG	CGGCGCGGCG	CGGCGCGGCG	CGGCGCGGCG	720
TGGTGGTGGT	GAGGCGGTTA	GGGCGGTTTC	CGGCGGTTTC	GGGCGGTTTC	CGGCGGTTTC	780
CGGCGGTTTC	GTGCGGTTAC	AGGCGGTTTC	CGGCGGTTTC	GGGCGGTTTC	CGGCGGTTTC	840
TGCGCGGTTT	CGGCGGTTTC	CGGCGGTTTC	CGGCGGTTTC	CGGCGGTTTC	CGGCGGTTTC	900
CGGCGGTTTC	CGGCGGTTTC	CGGCGGTTTC	CGGCGGTTTC	CGGCGGTTTC	CGGCGGTTTC	913

(2) INFORMATION FOR SEQ ID NO:17:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1872 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAGTACGTTG	GTGTAGAAAA	ATGCTGCGCG	CGGACCGCTT	AAGGCTGGGA	CAATTTCTGA	60
TAGCTACCGG	GACACAGGAG	GTACGCGGAT	GAGCAATTTC	CGGCGCGGCT	CAGTCAGGTC	120

GTGATGGTGG	CTGACGGTGC	TGGCTGCGGT	CGGGCTGGGC	CTGGCCACGG	CGCCGCCCCA	180
GGCGGGCCCG	CGGGCTTTGT	GGCAGGACGG	GTTCGCGGAC	TTCCCGCGCG	TGCCCCGTGA	240
CCCGTCGGCG	ATGGTCGGCC	AAGTGGCGCC	ACAGGTGGTC	AACATGAAAC	CGAACTGGGG	300
CTACACAAAC	GGCGTGGGCG	CGGGACCGCG	CATCGTCATC	GATCCCAACG	GTGTGCTGCT	360
GACCAACAAAC	CACCTGATCG	CGGGCGCCAC	CGAGATCAAT	GGCTTCAGCG	CGGCTCGCGG	420
CCAAACCTAC	GGCGTGGATG	TGGTGGGGTA	TGACCGGACC	CAGGATGTGC	CGGTGCTGCA	480
CTGTGCGCGT	GGCGTGGGCG	TGCGGTGGCG	GGCGATCGGT	GGCGCGGTGC	CGGTGCTGGA	540
GGCGGTGGTC	GGGATGGGCG	ACAGCGGTGG	GCAGGGCGGA	ACGCCCCGTC	CGGTGCTGGG	600
CAGGTTGGTC	GGGCTCGGCG	AAACCGTGCA	GGCGTGGGAT	TGCGTGACCG	GTGCGGAAGA	660
GACATGGAAC	GGGTGATGTC	AGTTCGATGC	CGCAATCCAG	CCCGGTGATT	CGGCGTGGCC	720
CGTCTGCAAC	GGCTAGGAC	AGGTGGTCGG	TATGAACACG	GGCGGTGCGC	ATAAATCTCA	780
GCTGTCCGAG	GGTGGGCGGG	GATTGCGCAT	TGGATCGGG	CAGGCGATGG	CGATGCGCGG	840
CGAATTCGGA	TGCGGTGGGG	GGTCACCCAC	CGTTCATATC	GGGCTTACCG	CGTTCCTCGG	900
CTTGGGTGTT	GTGACAAACA	ACGGCAACCG	CGCACGAGTC	ACACCGGTGG	TGCGGAAGCGG	960
TGCGGCGGCA	AGTCTCGGCA	TGTCACCGCG	CGACGTGATC	ACCGCGGTGG	ACGGCGGTCTC	1020
GATCAACTCG	GGCACTCGGA	TGGCGGACCG	GGTTAAACGG	CATCATCGCG	GTGAGCTGAT	1080
CTCGGTGAAC	TGGCAAAACA	AGTCGGGCGG	CACCGCTACA	GGGAACGTGA	CATTGGGCGA	1140
GGGAGCGCGG	GGCTGATTTG	TGCGGATATC	CACCTCGCGG	CGGGCCAAAT	GGATTGGGCG	1200
CAGCGCGTAT	TGCGCGGTGA	GGCGCGGAGT	TGGGTCTGCG	TGCGCGGTGG	CATTGTGGAA	1260
GCAATGAGCG	AGGCGAACA	CAGCGTTGAG	CAGCGTCTCG	TGCGAGGCGAG	TTAGCTGGAAC	1320
GGCGGTGTGG	TGGAGCATTC	GGATGCCAAG	GACTTCGGCA	CGCGCGCGCG	CGTGGCGGCG	1380
GATCGAGCTG	GGTTTAAACA	CGCGGTCTTC	TACGAGGTCG	TGGTCCGGCG	GTGTCTTGAC	1440
GGCAGCGCGG	ACGGTTCGCG	CGATCTGGGT	GGACTCATCG	ATCGGCTGGA	CTACCTGCAAC	1500
TGGGTTCGGA	TGAGCTGTCAT	CTGTTGCGCG	CGTTCGTAGG	ACTCACCGTC	CGCGGACGCG	1560
GATTACGACA	TGCGGACTTT	CTACAAGGTG	CGGCCCGAAT	TGGGCACTGT	CGACGATTTG	1620
GTGCGCGTGG	TGCGACCGCG	TCACCGGCGA	GGTATCGCGA	TCATGACCGA	CTGTGTGATG	1680
AATCACACTG	CGGATCTGCA	CGCTGTGTTT	CAGGAGTCCC	GGCGCGGACG	AGACGAGCGG	1740
TACGGTGAAT	ATTACGTGTG	GAGCGACACG	ACCGGAGCGT	ACACCGAGCG	CGGATCATTC	1800
TTGCTTGACA	CGGAAGAGTC	GAACTGGTCA	TTGATCTGTC	TGCGCGGACA	GTTTCTACTG	1860
GCACCGATTC	TT					1872

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTTCGCGGAA	ACCTGATGCC	SAGGAACAGG	GTGTTCCCGT	GAGCCCGAGG	GGTTCGAGCC	60
CGCGCGCTCG	CGCGGAGATC	AGGCGATCGC	TTGATGCGAC	AAAAGGGTTG	ACCAGCGTGC	120
ACGTAGCGGT	CGGAAAGTCC	ACAGCTTCTC	GGGTATTACC	AGTGGCGATG		180
TGAGCTCGCG	GGCTAATCGG	CTGCGGCAAA	AGGGCGTATG	CACCTACACG	GACGAGCAGG	240
GTGTCCCGTT	TGCGGTACAA	GGCGCAACAA	TGTCGGTGAA	ACTGTTGCGA	GACTGAGACA	300
ATCTCGGCTC	GATTTCTGAA	CTGTCAACTT	CACCGGTGCT	CGATCTGCGC	GCTGGGGTGA	360
CGCAGCTGCT	CTTCGGTGTG	ACGAACCTCC	AAGCGCAAGG	TACCGAAGTG	ATAGACGGAA	420
TTTCGACCAAC	CAAAATACCC	GGGACCATCC	CGCGGAGCTC	TGTCAAGATG	CTTGATCTCT	480
GGCGCAAGAG	TGCAAGGGCG	GGGACCGTGT	GGATTGCGCA	GGACGCGCTG	CACGACCTCG	540
TGCGAGCGAG	CATCGACCTC	GGATCCGGGT	CGATTTCAGT	CAGCGAGTGC	AAATGGAACG	600
AACCGTCAAA	CTTCGACTAG	GGCGAAGTTG	CGTGACGCGG	TTGCTGGAAG	CGCGCTTGTG	660
AACGGTGTCA	ACGGCACCGG	AAACTGAGC	CGCTGACGCG	ATCTGGAAGT	TGACCGGCTA	720
GACCGGGCGG	TGGTGTGTTA	TTGTTCCGTT	GTTCGCGCTG	GTGGGACCGG	CGCGAGGTTC	780
CGGTCTTTGA	GGCGGTAGCT	GTGCGCTTTG	AGGGCGAGCA	CTTCAGCATG	GTGGAGCAGG	840

CGGTGATCA	TGGCGGAGC	AACGACGTC	TGGCGGAGC	AAACCTCGCC	CCAGCGGCGG	900
AAGGCTTAT	TGGAGCTGAC	GATCAAGCTG	GCGGCTCAT	ACCGGGAGGA	CACGAGCTGG	960
AAGAAGAGGT	TGGCGGCGTC	GGGCTCAAC	GGATGTATC	CGACTTCGTC	AACGAGCAGG	1020
AGCGGATAGC	GGCGAAACCG	GGTAGCTCG	GGCGGCGGTC	GTGAGCTCTG		1080
GGGACCGTG	CTACCCATTC	GGCGGCGGTC	GGGAGACGCA	CCCGATGACC	GGGCTGACAC	1140
GGCGGTATCG	CCAGGCGGAC	GGCAAGATGA	GTCTTCCCGG	TGCGAGGCGG	GGCCCAAAAA	1200
CAGGAGCTTA	TGGCGGCGCG	TGATGAATC	CAGGCTGCCC	AGATGTGCGA	TGGTGTGCGG	1260
TTTGAGGCCA	CGAGCATGCT	CAAGTGTGAA	CTCTTCCAC	GACTTCGCGA	CCGCGAAGCG	1320
GGCGGCGCGG	ATGCGGCGCT	CACGACCATG	GGACTCCCGG	GCTGACACTT	CCGCTGCGAG	1380
CGAGGCGGCT	AGGTATTCTT	CGTGGCTGCA	GTCTCGGCG	CGGGCGCGAT	CGGCGAGCGG	1440
GGACACTGAC	TCAGCGAGGG	TGGGAGCTTT	CAATGCTCTT	GT		1482

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCA	CGAGCGCGCG	ATACTTCTG	GGCGCGGCGC	GACCATAGTG	CTGAGGGGTT	60
CGTGTCTGGG	GGCAGCGCGG	GGGCGACGAC	GCTGAGCGGT	GAGGGGCTTG	AACAGCGCGA	120
CGGTGACTCG	TGTGCTGTGG	ACGCGACGAA	CGCGGCGGTC	GTTCGCTTAC	ACCGGGCTTT	180
CGCGTACGAA	ATCGGCTACA	TGGGGAAGAG	CGGACTGCGC	AGGATGTGCG	GGGAGAACCC	240
GGAGAACATC	TTCTTCTACA	TCAGCTTTTA	CAACGAGCGG	TAGCTGCGAC	CGCGGCGGCG	300
GGAGAACTTC	GATCGCGAGG	GGGTGCTGGG	GGTATCTTAC	CGTATCAAG	CGGCGACCGA	360
GCAACGCGCC	AACAGGCGGC	AGATCTTGGC	CTCGGCGGTA	GGGATGCGCG	CGGCGCTGCG	420
GGCAGCACAG	ATGCTGCGCG	CGGATGCGGA	TGTGCGCGCC	GACCTGTGGT	CGGTGACCGA	480
TGGGCGCGAG	GTAAACGCGC	ACGCGGTGGT	CATCGAGACC	GAGAAAGCTTC	GGCAGCGCGA	540
TCGGCGCGCG	GGCGTGGCGT	ACGTGACGAG	AGCGGTGGAG	AATGCTGCGG	GGCGGTGAT	600
CGCGGTGTCG	GACTGAGTGC	GGCGGCTGTC	CGAGCAGATC	CGACCGTGGG	TGCGCGCGAC	660
ATACCTCACG	TGGGCGACCG	ACGCGTTCGG	TTTTTCGCGC	ACTCGGCGCG	CGGTCGCTCG	720
TTACTTCAAC	ACCGAGCGCG	AATCCAGGTT	TGGTCCGCGT	TTTGGGAGGG	GTTCGCTGCG	780
TCGACGGGTC	AATATGAGCC	CATTGCGTGC	CGTCTGTTGG	CGGCGCGCGC	AGTTCACCGG	840
ATTGACAGAA	GGTGGGGGTT	TGCGCGCGAG	TAAGTT			876

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCCCCCGGG	GCTGCGAGAA	TTGCGACGGA	GAGACAAAAT	TCCAGCGGTT	AATGCGAGAA	60
CAGATTGATA	ACGAATTCAC	AGCGGACGAA	CAATATGTG	CGATCGCGGT	TTATTGCGAC	120
ACCGAAGAGC	TGCGCGAGTT	GGCGAAGCAT	TTTTACAGCC	AAGCGGTGGA	GGAACTGAAC	180
GCGCAATGTA	TGCTGTGTGA	ACACTGTGTC	GACGCGGACC	TTCTGTGTGA	AATTCCCGCG	240
GTAGACACGG	TGCGAAGACA	GTTCGACAGA	CGCGCGGAGG	CAGTGGCGCT	GGCGCTCGAT	300
CAGGACGCGA	CAGTACGCGA	CGAGTGTGCT	CGGCTGACAG	CGGTGGCGCG	CGACGAGGCG	360
GATTGCTGCG	CGGAGCGATT	CATGCGATGG	TGTTGCGAG	AACAGATGCA	AGAGGTGCGC	420

TTGATGGCAA	CCTCGGTGCG	GSTTGCOSAT	CGGGCCGGGG	CCAACTGT	CGAGCTAGAG	480
AACCTTCGTC	CACGTGAAGT	GGATGTGGCG	CCGGCCGCAT	CAGGCGCCCC	GCACGCTGCC	540
GGGGGCCGCC	TCTAGATCCC	TGGGGGGGAT	CAGCGAGTGG	TCCCTTCGCG	CCGCGCCTCT	600
TCCAGCCGAG	CCTTGGTGGC	SCCGGGGTGG	TGAGTACCAA	TCCAGGCCAC	CCCGACCTTC	660
CGGNAAAAGT	CGATGTCTTC	GTACTCATCG	ACGTTCCAGG	AGTACACCGC	CCGCGCCTGA	720
GCTGCCGAGC	GCTCAACGAG	TTGCGGATAT	TGCTTTAAGG	CAGGCAGTGA	GGGTCCCGAG	780
GCCTTTGCCC	CGACGCCGAT	GGCGGCACTG	CTGGTCAGGT	ATCGGGGGGT	CTTGGCGAGC	840
AACAACCTGC	SCAGGAGGGG	TGGAGCCGCC	CGGATCGGCA	GACCGGGGGG	CGGAAAACGA	900
CATCAACACC	GCACGGGATC	GATCTCGCGA	GGGGGGTGGC	GGAAATACGA	ACCGGTGTAG	960
GAGCGCCAGC	AGTTTGTTTT	CCACCAGCGA	AGCGTTTTCG	GGTCATCGGN	GGCCTTTAAG	1020
T						1021

(2) INFORMATION FOR SEQ ID NO:21:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(11) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGTGCCGAGC	AACGGAAGAA	CACAACCATG	AAGATGGTGA	AATCGATCGC	CGCAGGTCTG	60
ACCGCCGCGG	CTGCAATCGG	CGCCGCTGCG	GCCTGTGTGA	CTTCGATCAT	GGCTGGCGGN	120
CGGCTCGTAT	ACGAGATGCA	CGCGGTCTTC	TTGCGCCGCG	CAGTGGCGTT	GGACCCGAGN	180
TCCGCGCCTG	ANGTCCCGAC	CGCGCCCGAG	TGGACCAAGC	TGCTCAACAG	NCTGNCGAT	240
CCCAACGTGT	CGTTTGGAG	CAAGGAGAGT	CTGGTCCAGG	GNGGNATCGG	NGGNCAGCAG	300
GGGNGNATTC	GNCAGNACCA	A				321

(2) INFORMATION FOR SEQ ID NO:22:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 173 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(11) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTTATCGGT	TCCGCTTGGC	GACCGGTTTT	GGGNGCGGGT	GTTTAAACCG	CTCGGCCAGC	60
CGATCGACCG	GGCGGAGACG	GTGCACTCGG	ATACTCGGCG	CGCGCTGGAG	CTCCAGCGCG	120
CCTCGGTGTG	GNAACGGCAA	GGCGTGAAGG	AGCGGTTGNA	GACCGGATTC	AAGGCGATTC	180
ACGCGATGAC	CCCGATCGCG	CGCGGGCAGC	CGCAGCTGAT	CATCGGGGAC	CGCAAGACCG	240
GCAAAAACCG	CGGCTGTGTG	CGGACACCAT	CCTCAAAACA	CGCGGAAGAA	CTGGGATTC	300
GCTGATCTCC	AAGAAGCAGG	TGCGCTTGTG	TATACGTTGG	CCATCGGGCA	AGAAGGGGAA	360
CTTACCATCG	CCG					373

(2) INFORMATION FOR SEQ ID NO:23:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGACGGCGT	GATGGGATTC	CTGGGCGGGG	CGGGTCCGCT	GGCGGTGGTG	GATCAGCAAC	60
TGGTTACCGG	GCTGCCGCAA	GCGTGGTGGT	TTGCTCAGGC	AGCGGCTGGG	CGGGTGGTGT	120
TCGTTACGGC	CTGGTACGGG	TTGGCCGATT	TAGCCGAGAT	CAAGGCGGGG	GAATCGGTGC	180
TGATCGATGC	CGGTACCGGC	GCTGGGGGCA	TGGCGGCTGT	GCAGCTGGCT	CGCGAGTGGG	240
GCGTGGAGGT	TTTCTCACC	GCGAGCCGTG	GNAAGTGGGA	CACGCTGGCG	GCGATGNGGT	300
TTGACGACGA	NCATATGCG	NGATTCCGNC	ACATNGGAAG	TTCCGANGGA	GA	352

(2) INFORMATION FOR SEQ ID NO:24:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAATCCCGG	TTCAATCCGT	TCGACGAGCG	GCTGGCGATA	ATCGACGAAG	TGATCAAGCC	60
GGGCTGGCGG	GGGCTCATGG	GTACAGAGGA	GTAAATCAGCA	AGTTCTCTGG	TATATCCGAC	120
CTAGCTCTCA	GTTCCTTGCC	AGATCGGTTT	CGTACGCTCA	TCGCAATGAC	CGGTTCCGCT	180
GGCGCAGGCT	CATGCTGGCG	GCTGTGATCC	TGGCCACGGG	TGTGGCGGGT	CTCGGGGTGG	240
GGCGCCAGTC	GGGAGCCGAA	ACGCGCCCGG	TGGCCGACTA	CTACTGGTGG	CGCGGGCAGC	300
CTTTGGAGCC	GGCATGGGGG	GGCACTGGGG	ATCCCTACAC	CTGCCATGAC	GACTTCCACC	360
GGCAAGAGGA	CGGCCCCGAC	CACAGCGCGG	ACTACCCCGG	ACCCATCTCT	GAAGATCCCG	420
TGCTTGACGA	TCCGGGTGGT	GGCGCCCGCG	CGGCGGCTGC	CGGTGGCGCG	GCATAGCGCT	480
CGTTGACCGG	GGCGCATGAG	CGAATAGCGG	TATAAACCAG	GGCTGGCCCG	CGGCAAGCTA	540
CGACCCCGGG	CGGGGCGAGT	TTAGCGTCCC	GTGCCGATGG	ATCGGCGGCT	CGGATGACAG	600
AAATAGAGGG	ACGGTTTGGG	GAACGCGTGG	GAGGAGCGTT	GAAGGGGAAC	TGTATGAAAC	660
GGCGACAGCG	GCTGCACCAT	CGCATATGAC	AAGGTTGTTA	CCCGCACACC	CGTTCCGCGG	720
ATCTTG						726

(2) INFORMATION FOR SEQ ID NO:25:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCGACGAGG	ACGAACGTGG	GGCCCAACAC	GGCCTATGCG	TTGATGACGG	GGACCGGGAT	60
GCTCGCCGAG	CATATCCGAG	CATGCTGGGT	GGCCACTAGG	CGACCTTTTG	ACGACCGGGG	120
CTGCCCGATG	GGGCGCCGAT	GAAGTCATGG	CGCCGGGGCT	TGTGCACTTG	ATGAACCCGA	180
ATAGGGAACA	ATAGGGGGGT	GATTTGGCAG	TTCAATGTGG	GGTATGGGTG	GAAATCCAAAT	240
CGCGGGGCAT	GCTGGGCGCC	GACGAGGCTC	CGCGAGGCGG	GGCAGCCCGA	ATTCGGAGGG	300
AGCACTCAAT	GGCGGCGATG	AAGCCCGCGA	CGGCGAGCGG	TGCTTTGGAA	GCAACTAAGG	360
AGGGGCGCGG	CATTGTGATG	CGACTACCAAC	TTGAGGGTGG	CGGTGCGCTG	GTCGTGAGGC	420
TGACACCCGA	CGAAGCGGCC	CGACTGGGTT	ACGAACCTAA	AGGCGTTACT	AGCTAAGAGC	480
AGCCCAACGG	CGAATGGGTG	GCTTACGGCG	CACACCTTCC	GGTAGATGTC	CAGTGTCTGC	540
TCGGCGATGT	ATGCCGAGGA	GAACCTGTGG	ATACAGCGGT			580

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACGGAGGCG	CGGGGGTTT	TGGGGGGCC	GGGGGGTCC	CGGGCAACGG	CGGGGGGGCC	60
GTTACCGCG	GGTGTTCGG	TGTGGCGCG	GGGGTGGGG	CGGGAGGCAA	CGGCATCGCC	120
GGTGTACGG	GTACTTGGG	CAGCACACCG	GGTGGATCCG			160

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACACCGATA	CGATGGTGT	GTACGCCAAC	GTGTTCGACA	CGCTCGAGGC	GTTCACGATC	60
CAGCGCACAC	CGACCGGGT	GACCATCGGC	GATGCGGGCC	CGTTCGGGGA	GGCGGCTGCC	120
AAGCGGATGG	GAATCGACAA	GTTGCGGGTA	ATTTCATACG	GAATCGACCG	CGTGTGTGCT	180
GAACGCGAAC	AGTGGGACGA	CGGCAACAC	ACGTTGGCGT	TGGCGCCCGG	TGTGTTGTC	240
GGCTACGAGC	GCACGTACA	GACCAACGCC	CG			272

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 317 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGAGCGGGTG	GTTCGCGAC	TATTCGGCA	CGGTACSCA	CGCGACGTC	CGCGAGCTGA	60
AGCGSATCGA	GCAGACGGAT	CGCTGCGGC	GGTTCATCG	CTACCTGGCC	GCTATCACCG	120
CGCAGGAGCT	GAACGTGGCC	GAAGCGGGC	GGTTCATCG	GTTCGACCG	GGGACGATCC	180
GTTCGGATCT	GGCGTGTTC	GAGACGCTCT	ATCTGGTACA	TGGCTGGCC	GCCTGGTGGC	240
GGAAATCTGAC	CGCGAAGATC	AAGAAGCGGT	CRAAGATCCA	CGTGTCTCAC	AGTGGCTTGC	300
CGGCGCTGTT	GGCGGGG					317

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCGTGGAG	CTGTGATGA	ACAGCCTTGC	CGGACGCGCG	CGGCGCAGCA	CGTCGGTGA	60
GCAGCGCGCG	ACCACCTTGC	CGGTGGGCG	CATGGTGATG	ACCACGTCG	CCTCGGCCAC	120
CGCTTCGGCG	CGGCTACGAA	ACACCGCGAC	ACCTTGGCGG	CGGCGCGCGG	ACGCGCGCGT	180
GG						182

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCGCGAAG	TTGGGTGAGC	AGGTGGTGG	CGGAAAGTC	TGGCGCGCTG	CGAAGCGGGT	60
CGGCGTTTAC	GAGCGGAGGA	CACGCTCTG	CGAGCTCTG	CGCTCTCTG	ACGCGCGGCA	120
GAGGTTGAGA	TTGCGCGCGG	CGGCGAGCGG	GTAGCAAGG	TTGCGCGCTG	GCATCTCTAT	180
GAGACTCGGC	GCTTAGGCAT	TGACCATGG	GTGTACGCG	TGCGCGAGCA	TTTGAGCGCT	240
CGGTTGTGAC	ACGAGCTGCT	CGAAGCTTT	CACCGGTGAA	CGGCTACCTG	ATCGACACCC	300
ACGTTTGG						308

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CGGACGAGCA	GCAACTCAGC	TGGATGATG	TGGGACGCG	CATTGAGGAC	GGGAGGATC	60
GGGCGGAGAC	TGCGCGCGCG	CAAGTCTCTA	TAGTGACGCG	CGGTAGAGGG	CTCGCGCGAT	120
GGGACCGGAC	TATTCGTGCG	TGCGCTTGG	CGGTAGAGG	GGGTAAAGGA	ATGTTAGGGG	180
ACACGATGAG	CAATCACACG	TACCGAGTGA	TGGATGATG	CGGACCTCG	CGGACGCGCG	240
TGACGCGCG	AATCCAGGCG	GGTCTGG				267

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTGCTCGCGA	AAGAATGTGA	GGGACACGA	TGAGCAATCA	CACCTACCGA	GTGATGAGA	60
TGCTCGGAGC	CTGCGCGGAC	GGGCTGAGC	CGGCAATCCA	GGGCGGTCTG	GCCGAGAGTG	120
CGGACAGCAT	CGGCGCGCTG	GACTGGTTTG	AAGTACAGTG	AATTCGAGGC	CACCTGGTGG	180
ACGAGCGCGT	CGGCGACTTC	CAGGTGACTA	TGAAAGTCTG	CTTGGCGCTG	AGGATTCTCT	240
AACCTTCAAG	CGGCGCGGAT	AAGTGGGTG	CATCATTAAG	CGACTTTTTC	AGAATCTCTT	300
GAGCGCGCTG	AAACGCGGCT	CAGCTGAGCG	TGGCTCGCGC	GAGGCGCTCG	CTTCAAAATC	360
CCTGCGAGAA	TTGCTCGCGG	GCGCTACAA	GGAAGTGGT	GCTGAATTCG	TGGGTATCTT	420

GGTCGACCTG	TGTGGGCTGC	AGCGGGACGA	AGCGGTGCTC	GACCTGGGCT	GCGGCTCGGG	480
GCGGATGGCG	TTGCCGCTCA	CGGGCTATCT	GAACAGCGAG	GGACGCTACG	CGGGCTTCGA	540
TATCTCGCAG	AAAGCCATCG	CGTGGTGCCA	GGAGCAGATC	ACCTCGGGCG	ACGCCCAATT	600
CCAGTTCCAG	GTCTCCGACA	TCTACAATCT	GCTGTACAAC	CCGAAAGGGA	AATGCCAGTC	660
ACTAGACTTT	CGCTTTCCAT	ATCCGATGCG	GTGCTTCGAT	GTGGTGTTC	TTACCTCGGT	720
GTTCAACCCAC	ATGTTTCCGC	CGGAAGTGGA	GCATATCTG	GACGAGATCT	CCCGGCTGCT	780
GAAGCCCGGC	GGAGGATGCT	TGTGCACGTA	CTTCTTGCTC	AATGACGAGT	CGTTAGCCCCA	840
CTTCGCGGAA	GGAAGAGATG	CGCACAACTT	CCAGCATGAG	GGACCGGGTT	ATCCGACAAT	900
CCACAGAAG	CGGCCCGAAG	AAGCAATCGG	CTTGGCGGAG	ACCTTCGTCA	GGGATGTCTA	960
TGGCAAGTTC	GGCTTCGCGG	TGCRGSAACC	ATTGCACTAC	GGCTCATGGA	GTGGCCCGGA	1020
ACCACGCCCTA	AGCTTCGAGG	ACATGCTCTT	CGGACCAAA	ACCGGAGGCT	AGGTCCGGAT	1080
CGGGGAAGCA	TGGGCACACC	GTGGCCCGGA	GCGCGGCTGC	CGGCAGGCGG	ATTAGCGGGG	1140
CAGATTAGCC	CGGCGCGGCT	CGCGGCTCCG	AGTACGGKGC	CCCGAATGGC	GTCAACGGCT	1200
GGTAACCCAG	CTTGCAGCGC	TGGCGGCGCG	CGTCCCGGAT	CAGGTGGTAG	ATGCCGACAA	1260
AGCTTCCGTC	ATCGGTCTATC	ACCAACGGTG	ACAGCAGCGG	GTGTGTCACC	AGCGCGAAGC	1320
CCACCCCGGT	CTCGGGGTCT	GTCCAGCGGA	TGAGCGCGCC	CAAGCCCACTA	TGACCAAAACC	1380
CGGGCATCAC	GTTCGCGATC	GGCATACCGT	GATAGCCAAAG	ATGAAATTTT	AAGGGCACCA	1440
ATAGATTTTC	ATCCGCGAGA	ACTTCCGCTC	GTTTCCCGGT	CAGGCGGGTG	ACCAGCTCCC	1500
CGACACAGAA	CGGTATGCGG	TGATCTCTGC	CTGTCGCG			1539

(2) INFORMATION FOR SEQ ID NO:13:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTGCAGGGTG	GCGTGGATGA	GCGTCACCGG	GGGGCAGGGC	GAGCTGACCG	CGGCCCAAGT	60
CGGGGTTCCT	CGGCGCGGCT	ACGAGAGCGG	GTATGGGCTG	ACGGTGCCCC	CGCGGTGTAT	120
CGCCGAGAAC	GCTGTGTAAC	TGATGATTCT	SATAGCGACC	AACCTCTTGG	CGCCAAACAC	180
CGCGCGATC	CGGGTCAACG	AGGCCGAATA	CGGCGAGATG	TGGGCCCAAG	ACGCCCGGCG	240
GATGTTTTGG	TACGCCGCGG	CGACGGCGAC	GGCGACGGCG	ACGTTGCTCG	CGTTTCGAGGA	300
GCGGCCGGAG	ATGACGAGCG	CGGCTGGGCT	CCTCGAGCAG	CGCGCCCGCG	TGAGGAGGCG	360
GTCCACACC	CGCGCGCGCA	ACCACTTGTAT	GAACAAATGT	CGCCAGGCGC	TGAACAGATT	420
CGCCAGCCCC	ACCGAGGGCA	CCAGGCTTTC	TTCCAGGCTG	GCTGGCCTGT	GGAAGACGGT	480
CTGCGCGCAT	CGGTGCGCGA	TGACGAACTAT	GCTGTGATG	GCCAAACAACC	ACATGTCGAT	540
GACCAACTCG	GCTGTGTGGA	TGACCAACAC	CTTGAGCTCG	ATGTTGAAGG	GCTTTGCTCC	600
GCGCGCGGCG	CGCCAGGCGG	TGCAAAACCG	GCGCCAAAC	GGGTTCGGCG	CGATGAGCTC	660
GCTGTGCGAG	TGCTTGGGTT	CTTCGGGCTC	GGCGGGTGGG	GTGGCGCGCA	ACTTGGTCTG	720
GCGCGGCTCG	GTACGGTATG	GTACCGGGGA	TGGCGGAAAA	TATGCANAGT	CTGGTCGGCG	780
GAACGGTGGT	CGGGGTAAAG	GTTCAGCCCC	GTTCCTCGGA	TGCGGTGAAC	TTCCTCAAGC	840
GAACAGATTA	C					851

(2) INFORMATION FOR SEQ ID NO:14:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GATCGATCGG	GGGGAATTT	GGACGAGTT	GGCTCCGGC	GATACCCAA	TCAATCGAAC	50
CTAGATTAT	TGGCTCCAGG	GGCCCGAGTA	ATGGCTCGCA	GGAGAGGAAC	CTTACTGCTG	120
CGGGACCTG	TCGTAGGTCC	TGATACGGC	GGAGGGGCTC	GACATTTTCC	ACCGACACCC	180
CCATCCAAAC	GTTCGAGGGC	CAGTCCAGCT	TGTGAGGGAG	GGACCCAGT	CGCAGGCTGC	240
GGTTGGGCA	GATC					254

(2) INFORMATION FOR SEQ ID NO:35:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCGTACG	GAAGCGGGG	CGCCCAAGGC	GAAGTGGCTG	TTGGACCGAG	AGGGACGGGA	50
CGATCTGGCG	CTGGCGATCG	CGGTTGAGCG	GGGGGGGGTG	GCTGGATTGC	GCTATAAGCT	120
TTTCTTCGAC	GACCCGACGC	TGGATGGTGA	CCAAACCGCG	GAGTTCGGTG	GTGTGAGGTT	180
GATCGTGGAC	CGGATGAGCG	CGGCTTATGT	GGAGGGCGCG	TGGATCGATT	TGCTGACAC	240
TATTGGGAAG	CAAGGTTTAC	CATCGACAAT	CCCAACGCCA	CGGGCTCGTG	CGGCTCCGGG	300
GATTCTGTCA	ACTGATAAAA	CGGTAGTACG	ACCCCGCGGT	CGGCAACACG	TACGAGCACA	360
CCAAGACCTG	ACCCGCTGTG	AAAGCACT	GAGCGATGCC	TTCGACTTGA	CGGCTGGGCG	420
GGCGCGCGGC	GGCAGGTGTC	ACTTGCATCG	TGAACAGCAC	CTGGGCTTGA	TATTGGGACC	480
AGTACAGGAT	TTTTTGGATG	GAGGTCACTT	CGAGCTGGGA	GAAGTCTCTG	CGGAACCGGT	540
CGCTCTCGAG	CTTGGGCAAG	GGCTGATCGG	AGGGCTTGTG	GGCAGCGCGG	TGCTGGATAC	600
GGCAGACGCG	ATTGCGAAGC	ATGGTGTGCA	CATCGCGGTT	CTCGACCGCG	TTGAGGTATC	660
CTTGAATCGC	GGTTTGGGCT	GGTCCCTGCG	AGAAATGTGC	TGCGCTGTTC	GCTCGTTTGG	720
TGCGGACCGC	GTATATGATC	GGCCCGCTCA	TAGCTGACAC	CAGCGCGAGG	GCTACACAGA	780
TGCGGATCG	CAGCGGCTTG	TGCGCTGCTT	TGGGTAGGA	CAGCTCGCGC	GGCAGCGCGG	840
GATATCGCGC	GGCCCGGCAG	GGCGGCTGCT	CTGCGGCTGC	GGGGGCGAAG	CGCGGTTGCG	900
CGCGCGCGAG	GTCTGGGGGG	TAGTCCAGGG	CTTGGGTTTC	GTGGGATGAG	GGCTCGGGGT	960
ACGGGCTGGG	TGCGTTGGTG	CGGACACCGG	GTTTCGGCGA	GTGGGAGACC	GGCATTTGTC	1020
TTCTCTTAGG	GTGGTGGGAC	GGACAGCTTG	CTAGGGCGAC	AACCGCGCGT	CGGCTGAGCC	1080
GGCAGCATCG	GCAATCAGGT	GAGCTCCCTA	GCGAGGCTAG	CGCAACAGCT	GCGCTGAGCT	1140
CTCAACCGGA	CGCGGCGCGC	CGCGGCGCGG	ATAATGTGGA	AAAGACTAGG	AACCTTAGGA	1200
ACGAAGGAGC	GAGATTTTGT	GACGATC				1227

(2) INFORMATION FOR SEQ ID NO:36:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGCGTGTGCG	CGGATCGGCG	GGGTGGTGA	ACGGCAACGG	CGGGCGCGCG	GGGGCGCGCG	50
GGACCGCGCG	TAACGCTGCT	CGCGGCGGCA	ACGCTGCTTT	GTTCGGGGCG	GGGGGCTGCG	120
CGCGGCGCGG	CACCAATGCT	GGGTGCGCG	GGTCCGCGCG	ATTGTGCTAC	GGCAACCGCG	180
						181

(2) INFORMATION FOR SEQ ID NO:37:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 290 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGGTGTCCGG	CGGATCCGGC	GGGTGGTTGA	ACGGCAACGG	CGGTGTCCGC	GGCCGGGGCG	60
GGGACGGCGT	CTTTGCGGGT	GGCGCGGCC	AGGGCGGGCT	CGGTGGGCAG	GGCGGCATG	120
GGGGCGGCTC	CACCGCGCGC	AACGGCGGTC	TTGGCGGGCG	GGCGGTGGC	GGAGGCAACG	180
GGCGGACGG	CGGCTTCGGT	GGCAACGGCG	GTAAGGGTGG	CCAGGGCGGN	ATTGGCGGGG	240
GCACTCAGAG	GGCGACCGCG	CTCGGNGTG	ACGGCGGTGA	CGCGGTGAC		290

(2) INFORMATION FOR SEQ ID NO:38:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GATCCAGTGG	CATGGNGGGT	GTCACTGGAA	GCAAT	34
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(2) INFORMATION FOR SEQ ID NO:39:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCGTGGT	GTTCCCGCC	TTGCCCGCGA	CGCCACCGGT	CCACCGTTA	CGAACACAGC	60
TGGCTTGGTC	GGCAGCACCC	CGCGACCGC	CGACCGCGGA	GTGCAACAAT	GGCACCGTGG	120
TATCCCGACC	ATTGGCGGCG	GNCCACCGG	CACCG			193

(2) INFORMATION FOR SEQ ID NO:40:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGGGGTTCA	CGGGGGCGCG	GGGACCGGGC	AGCCCCGNGG	GGCCGGGGGG	TGG	53
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(2) INFORMATION FOR SEQ ID NO:41:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCCACCGG	GGGTGCAGAC	GGTCCCGCG	GGCCACCCG	GACCAGCGCG	GGCAACGGCG	60
GCACGGGGGG	CAACGGGGCG	AACGCCACCG	TCTCGGNGG	GGCCGCGCG	GCCGCGGGCA	120
AGGGCGGCAA	CG					132

(2) INFORMATION FOR SEQ ID NO:42:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCGGGCG	CGGNACGGNG	GGGACGGCG	GCAAGGGCGG	NAACGGGGCG	GGCGNACCGA	60
CCNACCAAGA	ATCTTCGGNG	TCNCCCAATG	GGCGAATGG	CGGACAGGGG	GGCAACGGCG	120
GCANCGGGCG	CA					132

(2) INFORMATION FOR SEQ ID NO:43:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 702 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCAGGAGG	ATCGGTACCC	CGCGCATCG	GCAGTACCG	ATTCCCGGG	TTTCCCGACC	60
CGAGGAAAGC	CGGTACCCAGA	TGGCGCTGCC	GAAGTAGGCG	GATCCGTTCC	CGATCGCGGC	120
ATGAACGGGC	GGCATCAAAT	TAGTGCAGGA	ACCITTCAGT	TTAGCGACGA	TAATGGCTAT	180
AGCACTAAGG	AGGATGATCC	GATATGACCG	AGTCCGACAG	CGTGACGGTG	GATCAGCAAG	240
AGATTTTGAA	CAGGGCCCAAC	GAGGTGGAGG	CCCGGATGGC	GGACCCACCG	ACTGATGTCC	300
CGATCAGACC	GTGCGAATTC	ACGGNGGNTA	AAAACCGCGC	CCAACAGNTG	GTNTTGTCCG	360
CCGACAACAT	CGCGGAATAC	CTGGCGCGCG	GTGCCAAAGA	CGGCGAGCGT	CTGGCGACCT	420
CGCTGCGCAA	CGCGGCCCAAG	GGGTATGGCG	AGGTTGATGA	GGAGGCTCGG	ACCGCGCTGG	480
ACAACGACGG	CGAAGGAACT	GTGCGAGGCG	AATCGGCCGG	GGCCGTTCGA	GGGGACAGTT	540
CGGCCGAAT	AACCATACG	CCGAGGCTGG	CCACGGCGCG	TGAACGCCAC	TTGATGGATC	600
TCAAAGAAGC	GGCAAGGAAG	CTGAAACCG	CGGACCAAGG	CGCATGGCTC	CGGCGACTGG	660
GGGATGGGTG	GAACACTTNC	ACCTTGACGC	TGCAGGCGCA	CG		720

(2) INFORMATION FOR SEQ ID NO:44:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 298 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAAGCCGCGAG	GCTGTCTGGG	CGACGTGGCG	GTCAAAGCGG	CATCGCTCGG	TGGCGGTGGA	60
GGCGCGCGGG	TGCGGTGGG	GCGGTGGGA	TCTCGGATCG	GGGCGCGCGA	ATCGGTGCGG	120
CCCGCTGGCG	CTGGTACAT	TGCGGCTTA	GGCGAGGAA	GGGCGCGCGG	CGCGCGCGCG	180
CTGCGCGCGG	GTGGCATGGG	AATGCGGATG	GTTGCCGCGC	ATCAGGGACA	AGGGGGCGCG	240
AAGTCCAAAG	GTTCTCAGCA	GGAAGACGAG	GCGCTCTACA	CGAGGATCC	TGCTGCGG	298

(2) INFORMATION FOR SEQ ID NO:45:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGCACGAGG	ATCGAATGCG	GTGCGCGGGA	GCACAGCGTC	GCAGTGCACC	AGTGGAGGAG	60
CGATGACCTA	CTGCGCGGGT	AACCGCGGAT	ACCCGCAAGC	GCAGCGCGCA	GGCTCCTACG	120
GAGCGCTAC	ACCGCTGCTC	CGCCACGCGG	ATGAGGGTGC	GAGCAAGCTA	CGGATGTACC	180
TGAACATCGC	GGTGGCAGTG	CTGCGCTGCG	CTGCGTACTT	CGCCAGCTTC	GGCCCCATGT	240
TGACCTCTAG	TACCGAATCT	GGGCGGGGTG	ATGGCGCAGT	GTCCGGTGAC	ACTGGGCTGC	300
CGGTGCGGGT	GGCTCTGCTG	GCTGCGCTGC	TTCGCGGGGT	GTTCTTGCTG	CGTAAGGCCA	360
AGAGCATGT	GACGTAGATT	CGGTTGCTCG	GGGTACTGCG	CGTATTCTCG	ATGGTCTCGG	420
CGACGTTTAA	CAAGCCGACG	GCGTATTGGA	CGGTTGGGCG	ATTGTGGGTT	GTGTTGGCTT	480
TGATCTGTTT	CGAGCGGGTT	GCGGCGAGTC	TGGCGCTCTT	GTTGGAGACC	GGCGCTATCA	540
CCGCGCGCGC	CGCGCGCGCT	AGGTTGAGCT	CGTATGAGCA	GTACGGGCGG	TACGGGCAGT	600
ACGGGCGAGT	CGGGGTGCGG	CGGGTGGGT	ACTACGCTCA	GCAGGGTGCT	CAGCAGCGCG	660
CGGGACTGCA	GTGCGCGCGG	CGGCAGCAGT	CTCGGCAGCC	TCCGGGATAT	GGGTGCGCAGT	720
ACGGCGGCTA	TTCGTTCCAGT	CGGAGCGCAAT	GGGGCAGTGG	ATACACTGCT	CAGCGCGCGG	780
CTCAACCGCC	GGGCGAGTGC	GGGTGCGCAAC	AATCGCACTA	GGGCGCATCC	ACGCCACCTA	840
CGCGCTTTCC	GAGGTTACGC	CGACCACTAC	CGGTGAGTGC	CGGGACGCGG	TGCGAGGCTG	900
GTTGCGCTGC	AGTCAACTAT	TCAACCGCCA	GGGCGGCGGA	CGAGTCTGCG	TCCCCCGGGG	960
GGGCGCGGGT	CTAACCGGCG	GTTCCCGCGT	CGGATCGCGC	GTGTGCGCGA	AGAGTGAACA	1020
GGGTGTCAGC	AAGCGCGGAC	GATCTCTGCT	CGGAATTG			1058

(2) INFORMATION FOR SEQ ID NO:46:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGGCACGAGA	GACCGATGCC	GCTACCGTGC	CGCAGGAGCG	AGGTAATTTC	GAGCGGATCT	60
CGGGCGGACT	GAAACACCGG	ATCGACCAAG	TGGAGTGCAG	GGCAGGTTCC	TTCAGGGGCG	120
AGTGGCGCGG	CGCGGCGCGG	ACGCGCGCGC	AGGCGCGGGT	GTTGCGCTTC	CAAGAAGCAG	180
CGAATAGCA	GAGCGAGGAA	CTCGACGAGA	TCTGACGAAA	TATTCTTCAG	SCCGGCGTCC	240
AATAGTCCAG	GGCGGACGAG	GAGCAGCAGC	AGGCGCTGTC	CTCGCAATG	GGCTTCTGAC	300
CGGTAATAC	GAAAGAAGAA	GGGCGCA				327

(2) INFORMATION FOR SEQ ID NO:47:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGGTGCGGAT GATGGCGGTG TCGAAGCTGA CCGATTCTGT ACCGCCGTGG TTGAGATCAA	60
CCAACACGCT GTTGGCGGTG GCAAAATGTGC CGNACCCGTG GATCTCGGTG ATCTTGTTCT	120
TCTTCATCAG GAAGTGCACA CGGCCACCC TGCCTCGGN TACCTTTGGG	170

(2) INFORMATION FOR SEQ ID NO:48:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCCGCGG CACGGGGGTT GCGCGCGCA GCAACGCTGG CGTGGCGGC AACGGCGGG	60
CGCGCGGTG CGCGGAACG GTTGGGTTC TCTTCGCAA CGCGGTGCT GCGCGGCAG	120
CGCGCT	127

(2) INFORMATION FOR SEQ ID NO:49:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGCGCGCAG GCGGCACG CGGCCAAGG GAGCGCGCG CGCGCGGCA ACGCGGCNA	60
CGCGCGCTCC GCGCTCAAG G	81

(2) INFORMATION FOR SEQ ID NO:50:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCAGGCT GCGCGGCTCC GCGCAGAAG GCGTACCG AGGAGCTGCC GGATTSTTT	60
GCAACGCGG GCGCGGCT GCGCGCGCT CCAACCAAG CGGTACCGC GCGCGCGCG	120
GAACGCTG TCGCGGTGG CTGATCTG	149

(2) INFORMATION FOR SEQ ID NO:51:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGACGAGAGA TCACACCTAC CGAGTGATG AGATCGTCGG GACCTCGCCC GACGGTGTGG	60
ACCGGHNAT CCAGGGCGGT CTGGCCCGAG CTGCGCAGAC CATCGCCGG CTGGACTGGT	120
TCGAAGTACA GTCAATTGGA GGCACCTGG TCGACGGAGC GGTGCGCCAC TTCAGGTGA	180
CTATGAAGT CGGCTTCGCG CTGGAGGATT CTTGAACCTT CAAGCGCGCG CGATAACTGA	240
GGTGCAATCAT TAAGCGGACTT TTCCAGAACCA TCTTGACCGG CTGGAACCGC GGTTCAGCGC	300
ACGGTGTGCTC CGCCGAGGCG CTGGCTCGAA AATCGCTGG ACAATCTGTC GCGCG	355

(2) INFORMATION FOR SEQ ID NO:52:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 999 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCATCAC ATCACATCA CATGCATCAG GTGGACCCCA ACTTGACAG TCGCAAGGGA	60
CGATTGGGCG CACTGGCTAT GCGCGCGATG GCGAGCGCCA GCTTGGTAC GATTGCGGTG	120
CCCGCGACCG CCACAGCCGA TCGGAGGCCA GCGCCCGCGG TACCCACAGC GCGCGCTCG	180
CCGCGCTCGA CGGCTGCGAG GCGACCGGCA CGCGCGACAC CTGTTGCCCC CCGACACCG	240
GCGCGCGCCA ACACCGCGAA TGCGCGAGCG GCGGATCCCA AGCGAGCACC TCGCGCGCG	300
GACCGCAACG CACCGCGCGC ACCTGTCTAT GCGCGAACCG CACCGCGAAC TGTGCGGATC	360
GACAACCGCG TTGGAGGATT CAGCTTCGCG CTGCTTGTCT GCTGGGTGGA GTCTGACCGC	420
GCGCACTTGG ACTACGTTTC AGCACTTCTC AGCAAAACCA CCGGGGACCC GCCATTTC	480
GGACAGCGCG CCGCGGTGGC CAATGACACC CGTATGTTG TCGGCGCGCT AGACCAAAAG	540
CTTTACGCCA GCGCGCGAAG CACCGACTCC CGTATGTTG TCGGCGCGCT AGACCAAAAG	600
GGTGAGTTCT ATATGCGCTA CCGGGGACCC CGGATCAGC AGGAAACCGT CTGCGTGGAC	660
GCGCAACCGG TGTCTGGAGG CGCTCTGTAT TACGAAGTCA AGTTCAGCGA TCCGAGTAA	720
CGGAACCGCG AGATCTGGAC GCGCTTAATC GCGCTGCGCG CCGCGAAGCG ACCGCGACCG	780
GCGCGCGCTC AGCGCTGGTT TGTGATAGG CTCGGGACCG CCAACAACCG GGTGGACAG	840
GCGCGCGCCA AGCGCTGGCT GGAATGGATC GCGCTTTGG TCGCGCGCGC GCGCGCGCG	900
GCAACCGCTC CTGCAAGAGC CGCTCGCGCG CCGCGCGCGG CCGGGGAAGT CGCTCTTACC	960
CGGACGACAC CGACACCGCA GCGGACTTGA CCGGCTTGA	999

(2) INFORMATION FOR SEQ ID NO:53:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
 1 5 10 15
 Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
 20 25 30
 Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
 35 40 45
 Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
 50 55 60
 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
 65 70 75 80
 Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
 85 90 95
 Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Val Ile Ala Pro
 100 105 110
 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
 115 120 125
 Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
 130 135 140
 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
 145 150 155 160
 Gly Gln Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
 165 170 175
 Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
 180 185 190
 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
 195 200 205
 Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
 210 215 220
 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
 225 230 235 240
 Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
 245 250 255
 Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
 260 265 270
 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
 275 280 285
 Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
 290 295 300
 Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
 305 310 315 320
 Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
 325 330

(2) INFORMATION FOR SEQ ID NO:54:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(3) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Asn Tyr Gly Gln Val

1	5	10	15
Val Ala Ala Leu			
20			

(2) INFORMATION FOR SEQ ID NO:55:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala	Val	Glu	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:56:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Glu	Ala	Ala	Lys
1				5					10						15
Glu	Gly	Arg													

(2) INFORMATION FOR SEQ ID NO:57:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr	Tyr	Trp	Cys	Pro	Gly	Gln	Pro	Phe	Asp	Pro	Ala	Trp	Gly	Pro
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:58:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO:60:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Ala Ala Ala Ala Pro Pro
 1 5 10 15
 Ala

(2) INFORMATION FOR SEQ ID NO:61:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Gln Thr Ser
 1 5 10 15

Leu Leu Asn Asn Leu Ala Asp Pro Asp Val Ser Phe Ala Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Thr Gly Ser Leu Asn Gln Thr His Asn Arg Arg Ala Asn Glu Arg Lys
 1 5 10 15
 Asn Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala
 20 25 30
 Ala Ala Ala Ile Gly Ala Ala Ala Gly Val Thr Ser Ile Met Ala
 35 40 45
 Gly Gly Pro Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro
 50 55 60
 Leu Pro Leu Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln
 65 70 75 80
 Leu Thr Ser Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala
 85 90 95
 Asn Lys Gly Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg
 100 105 110
 Ile Ala Asp His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro
 115 120 125
 Leu Ser Phe Ser Val Thr Asn Ile Gln Pro Ala Ala Gly Ser Ala
 130 135 140
 Thr Ala Asp Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr
 145 150 155 160
 Gln Asn Val Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala
 165 170 175
 Ser Ala Met Glu Leu Leu Gln Ala Ala Gly Xaa
 180 185

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asp Glu Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu
 1 5 10 15
 Ser Glu Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu Ser Ala Val Ser
 20 25 30
 Gly Val Glu Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg
 35 40 45
 Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Ile Thr Ser

50	55	60
Ala Gly Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val		
65	70	75
Ser Arg Arg His Ala Glu Phe Arg Leu Glu Asn Asn Glu Phe Asn Val		80
	85	90
Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val		95
	100	105
Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Leu		110
	115	120
Arg Leu Val Phe Leu Thr Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser		125
	130	135
Thr Gly Gly Pro		140
145		

(2) INFORMATION FOR SEQ ID NO:65:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr Ser Asn Arg Pro Ala Arg Arg Gly Arg Arg Ala Pro Arg Asp Thr		
1	5	10
Gly Pro Asp Arg Ser Ala Ser Leu Ser Leu Val Arg His Arg Arg Gln		15
	20	25
Gln Arg Asp Ala Leu Cys Leu Ser Ser Thr Gln Ile Ser Arg Gln Ser		30
	35	40
Asn Leu Pro Pro Ala Ala Gly Gly Ala Ala Asn Tyr Ser Arg Arg Asn		45
	50	55
Phe Asp Val Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu		60
	65	70
Leu Cys Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Glu		75
	80	85
Glu Leu Lys Gly Thr Asp Thr Gly Gln Ala Cys Gln Ile Gln Met Ser		90
	95	100
Asp Pro Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp		105
	110	115
Gln Lys Ser Leu Glu Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu		120
	125	130
Ser Ala Ala Thr Ser Ser Thr Pro Arg Glu Ala Pro Tyr Glu Leu Asn		135
	140	145
Ile Thr Ser Ala Thr Tyr Gln Ser Ala Ile Pro Pro Arg Gly Thr Gln		150
	155	160
Ala Val Val Leu Xaa Val Tyr His Asn Ala Gly Gly Thr His Pro Thr		165
	170	175
Thr Thr Tyr Lys Ala Phe Asp Trp Asp Gln Ala Tyr Arg Lys Pro Ile		180
	185	190
Thr Tyr Asp Thr Leu Trp Gln Ala Asp Thr Asp Pro Leu Pro Val Val		195
	200	205
Phe Pro Ile Val Ala Arg		210
215		220
225		

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Glu Gly Gly Gln Gly Phe
1          5          10          15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20          25          30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35          40          45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50          55          60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65          70          75
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85          90          95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100         105         110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115         120         125
Gly Pro Pro Ala
130

```

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Val Pro Leu Arg Ser Pro Ser Met Ser Pro Ser Lys Cys Leu Ala Ala
1          5          10          15
Ala Gln Arg Asn Pro Val Ile Arg Arg Arg Leu Ser Asn Pro Pro
20          25          30
Pro Arg Lys Tyr Arg Ser Met Pro Ser Pro Ala Thr Ala Ser Ala Gly
35          40          45
Met Ala Arg Val Arg Arg Arg Ala Ile Trp Arg Gly Pro Ala Thr Xaa
50          55          60
Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val
65          70          75
Ile Gln Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly
85          90          95
Ser Glu Arg Lys
100

```

(2) INFORMATION FOR SEQ ID NO:68:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Met Thr Asp Asp Ile Leu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr
1      5      10      15
Leu Thr Leu Asn Arg Pro Gln Ser Arg Asn Ala Leu Ser Ala Ala Leu
20     25     30
Arg Asp Arg Phe Phe Ala Xaa Leu Xaa Asp Ala Glu Xaa Asp Asp Asp
35     40     45
Ile Asp Val Val Ile Leu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly
50     55     60
Leu Asp Leu Lys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly His Leu
65     70     75     80
Thr Ala Val Gly Gly His Asp Gln Ala Gly Asp Arg Arg Asp Gln Arg
85     90     95
Arg Arg Gly His Arg Arg Ala Arg Thr Gly Ala Val Leu Arg His Pro
100    105    110
Asp Arg Leu Arg Ala Arg Pro Leu Arg Arg His Pro Arg Pro Gly Gly
115    120    125
Ala Ala Ala His Leu Gly Thr Gln Cys Val Leu Ala Ala Lys Gly Arg
130    135    140
His Arg Xaa Gly Pro Val Asp Glu Pro Asp Arg Leu Pro Val Arg
145    150    155    160
Asp Arg Arg

```

(1) INFORMATION FOR SEQ ID NO:69:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Met Lys Phe Val Asn His Ile Glu Pro Val Ala Pro Arg Arg Ala Gly
1      5      10      15
Gly Ala Val Ala Glu Val Tyr Ala Glu Ala Arg Arg Glu Phe Gly Arg
20     25     30
Leu Pro Glu Pro Leu Ala Met Leu Ser Pro Asp Glu Gly Leu Leu Thr
35     40     45
Ala Gly Trp Ala Thr Leu Arg Glu Thr Leu Leu Val Gly Gln Val Pro
50     55     60
Arg Gly Arg Lys Glu Ala Val Ala Ala Ala Val Ala Ala Ser Leu Arg
65     70     75     80
Cys Pro Trp Cys Val Asp Ala His Thr Thr Met Leu Tyr Ala Ala Gly
85     90     95
Gln Thr Asp Thr Ala Ala Ala Ile Leu Ala Gly Thr Ala Pro Ala Ala
100    105    110

```

Gly Asp Pro Asn Ala Pro Tyr Val Ala Trp Ala Ala Gly Thr Gly Thr
 115 120 125
 Pro Ala Gly Pro Pro Ala Pro Phe Gly Pro Asp Val Ala Ala Glu Tyr
 130 135 140
 Leu Gly Thr Ala Val Gln Phe His Phe Ile Ala Arg Leu Val Leu Val
 145 150 155 160
 Leu Leu Asp Glu Thr Phe Leu Pro Gly Gly Pro Arg Ala Gln Gln Leu
 165 170 175
 Met Arg Arg Ala Gly Gly Leu Val Phe Ala Arg Lys Val Arg Ala Glu
 180 185 190
 His Arg Pro Gly Arg Ser Thr Arg Arg Leu Glu Pro Arg Thr Leu Pro
 195 200 205
 Asp Asp Leu Ala Trp Ala Thr Pro Ser Glu Pro Ile Ala Thr Ala Phe
 210 215 220
 Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro
 225 230 235 240
 Thr Arg Gln Val Val Arg Arg Val Val Gly Ser Trp His Gly Glu Pro
 245 250 255
 Met Pro Met Ser Ser Arg Trp Thr Asn Glu His Thr Ala Glu Leu Pro
 260 265 270
 Ala Asp Leu His Ala Pro Thr Arg Leu Ala Leu Leu Thr Gly Leu Ala
 275 280 285
 Pro His Gln Val Thr Asp Asp Asp Val Ala Ala Ala Arg Ser Leu Leu
 290 295 300
 Asp Thr Asp Ala Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr
 305 310 315 320
 Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Glu Gly Gln
 325 330 335
 Val Ser Arg Gln Asn Pro Thr Gly
 340

(2) INFORMATION FOR SEQ ID NO:70:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 495 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asp Asp Pro Asp Met Pro Gly Thr Val Ala Lys Ala Val Ala Asp Ala
 1 5 10 15
 Leu Gly Arg Gly Ile Ala Pro Val Glu Asp Ile Gln Asp Cys Val Glu
 20 25 30
 Ala Arg Leu Gly Glu Ala Gly Leu Asp Asp Val Ala Arg Val Tyr Ile
 35 40 45
 Ile Tyr Arg Gln Arg Arg Ala Gln Leu Arg Thr Ala Lys Ala Leu Leu
 50 55 60
 Gly Val Arg Asp Glu Leu Lys Leu Ser Leu Ala Ala Val Thr Val Leu
 65 70 75 80
 Arg Glu Arg Tyr Leu Leu His Asp Glu Gln Gly Arg Pro Ala Glu Ser
 85 90 95
 Thr Gly Glu Leu Met Asp Arg Ser Ala Arg Cys Val Ala Ala Glu
 100 105 110

Asp Gln Tyr Glu Pro Gly Ser Ser Arg Arg Trp Ala Gln Arg Phe Ala
 115 120 125
 Thr Leu Leu Arg Asn Leu Glu Phe Leu Pro Asn Ser Pro Thr Leu Met
 130 135 140
 Asn Ser Gly Thr Asp Leu Gly Leu Leu Ala Gly Cys Phe Val Leu Pro
 145 150 155 160
 Ile Glu Asp Ser Leu Gln Ser Ile Phe Ala Thr Leu Gly Gln Ala Ala
 165 170 175
 Glu Leu Gln Arg Ala Gly Gly Gly Thr Gly Tyr Ala Phe Ser His Leu
 180 185 190
 Arg Pro Ala Gly Asp Arg Val Ala Ser Thr Gly Gly Thr Ala Ser Gly
 195 200 205
 Pro Val Ser Phe Leu Arg Leu Tyr Asp Ser Ala Ala Gly Val Val Ser
 210 215 220
 Met Gly Gly Arg Arg Arg Gly Ala Cys Met Ala Val Leu Asp Val Ser
 225 230 235 240
 His Pro Asp Ile Cys Asp Phe Val Thr Ala Lys Ala Glu Ser Pro Ser
 245 250 255
 Glu Leu Pro His Phe Asn Leu Ser Val Gly Val Thr Asp Ala Phe Leu
 260 265 270
 Arg Ala Val Glu Arg Asn Gly Leu His Arg Leu Val Asn Pro Arg Thr
 275 280 285
 Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile
 290 295 300
 Cys Lys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp
 305 310 315 320
 Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala
 325 330 335
 Thr Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn
 340 345 350
 Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp
 355 360 365
 Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Asp
 370 375 380
 Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Gln Leu Gly Gln Ala
 385 390 395 400
 Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu
 405 410 415
 Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg
 420 425 430
 Leu Ala Thr Arg Leu Met Arg Arg Ile Gln Gln Ala Ala His Thr Ala
 435 440 445
 Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp
 450 455 460
 Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Gln Val Thr Ser
 465 470 475 480
 Val Ala Pro Thr Gly
 485

(2) INFORMATION FOR SEQ ID NO:71:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```

Gly Val Ile Val Leu Asp Leu Glu Pro Arg Gly Pro Leu Pro Thr Glu
1      5      10
Ile Tyr Trp Arg Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val
20      25      30
Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala
35      40      45
Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His
50      55      60
Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Gln Thr Glu
65      70      75
Gly Asn Ala Ala Ala Pro Pro Gln Gly Gln Asn Pro Glu Thr Pro
85      90      95
Thr Pro Thr Ala Ala Val Gln Pro Pro Pro Val Leu Lys Glu Gly Asp
100     105     110
Asp Cys Pro Asp Ser Thr Leu Ala Val Lys Gly Leu Thr Asn Ala Pro
115     120     125
Gln Tyr Tyr Val Gly Asp Gln Pro Lys Phe Thr Met Val Val Thr Asn
130     135     140
Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala
145     150     155
Ala Tyr Val Tyr Ser Leu Asp Asn Lys Arg Leu Trp Ser Asn Leu Asp
160     165     170
Cys Ala Pro Ser Asn Glu Thr Leu Val Lys Thr Phe Ser Pro Gly Glu
175     180     185
Gln Val Thr Thr Ala Val Thr Thr Thr Gly Met Gly Ser Ala Pro Arg
190     195     200
Cys Pro Leu Pro Arg Pro Ala Ile Gly Pro Gly Thr Tyr Asn Leu Val
205     210     215
Val Gln Leu Gly Asn Leu Arg Ser Leu Pro Val Pro Phe Ile Leu Asn
220     225     230
Gln Pro Pro Pro Pro Gly Pro Val Pro Ala Pro Gly Pro Ala Gln
235     240     245
Ala Pro Pro Pro Glu Ser Pro Ala Gln Gly Gly
250     255     260

```

(2) INFORMATION FOR SEQ ID NO:72:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val
1      5      10
Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu Val Val Ala
20      25      30
Gly Gly Ala Ala Asn Ala Gly Val Pro Lys Gly Val Val Val Thr
35      40      45

```

Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala
 50 55 60
 Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gln Asp
 65 70 75 80
 Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly Lys Ala Glu
 85 90 95
 Gln

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 364 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly Ala Ala Val Ser Leu Leu Ala Ala Gly Thr Leu Val Leu Thr Ala
 1 5 10 15
 Cys Gly Gly Gly Thr Asn Ser Ser Ser Ser Gly Ala Gly Gly Thr Ser
 20 25 30
 Gly Ser Val His Cys Gly Gly Lys Lys Glu Leu His Ser Ser Gly Ser
 35 40 45
 Thr Ala Gln Glu Asn Ala Met Glu Gln Phe Val Tyr Ala Tyr Val Arg
 50 55 60
 Ser Cys Pro Gly Tyr Thr Leu Asp Tyr Asn Ala Asn Gly Ser Gly Ala
 65 70 75 80
 Gly Val Thr Gln Phe Leu Asn Asn Glu Thr Asp Phe Ala Gly Ser Asp
 85 90 95
 Val Pro Leu Asn Pro Ser Thr Gly Gln Pro Asp Arg Ser Ala Glu Arg
 100 105 110
 Cys Gly Ser Pro Ala Trp Asp Leu Pro Thr Val Phe Gly Pro Ile Ala
 115 120 125
 Ile Thr Tyr Asn Ile Lys Gly Val Ser Thr Leu Asn Leu Asp Gly Pro
 130 135 140
 Thr Thr Ala Lys Ile Phe Asn Gly Thr Ile Thr Val Trp Asn Asp Pro
 145 150 155 160
 Gln Ile Gln Ala Leu Asn Ser Gly Thr Asp Leu Pro Pro Thr Pro Ile
 165 170 175
 Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln
 180 185 190
 Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser
 195 200 205
 Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly
 210 215 220
 Thr Ser Ala Leu Leu Gln Thr Thr Asp Gly Ser Ile Thr Tyr Asn Glu
 225 230 235 240
 Trp Ser Phe Ala Val Gly Lys Gln Leu Asn Met Ala Gln Ile Ile Thr
 245 250 255
 Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys
 260 265 270
 Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu
 275 280 285
 Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile

290	295	300
Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr		
305	310	315
Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly		320
	325	330
Gln Glu Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe		335
	340	345
Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser		350
	355	360

(2) INFORMATION FOR SEQ ID NO:74:

- (a) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gln	Ala	Ala	Ala	Gly	Arg	Ala	Val	Arg	Arg	Thr	Gly	His	Ala	Glu	Asp	1	5	10	15
Gln	Thr	His	Gln	Asp	Arg	Leu	His	His	Gly	Cys	Arg	Arg	Ala	Ala	Val	20	25	30	
Val	Val	Arg	Gln	Asp	Arg	Ala	Ser	Val	Ser	Ala	Thr	Ser	Ala	Arg	Pro	35	40	45	
Pro	Arg	Arg	His	Pro	Ala	Gln	Gly	His	Arg	Arg	Arg	Val	Ala	Pro	Ser	50	55	60	
Gly	Gly	Arg	Arg	Arg	Pro	His	Pro	His	His	Val	Gln	Pro	Asp	Asp	Arg	65	70	75	80
Arg	Asp	Arg	Pro	Ala	Leu	Leu	Asp	Arg	Thr	Gln	Pro	Ala	Glu	His	Pro	85	90	95	
Asp	Pro	His	Arg	Arg	Gly	Pro	Ala	Asp	Pro	Gly	Arg	Val	Arg	Gly	Arg	100	105	110	
Gly	Arg	Leu	Arg	Arg	Val	Asp	Asp	Gly	Arg	Leu	Gln	Pro	Asp	Arg	Asp	115	120	125	
Ala	Asp	His	Gly	Ala	Pro	Val	Arg	Gly	Arg	Gly	Pro	His	Arg	Gly	Val	130	135	140	
Gln	His	Arg	Gly	Gly	Pro	Val	Phe	Val	Arg	Arg	Val	Pro	Gly	Val	Arg	145	150	155	160
Cys	Ala	His	Arg	Arg	Gly	His	Arg	Arg	Val	Ala	Ala	Pro	Gly	Gln	Gly	165	170	175	
Asp	Val	Leu	Arg	Ala	Gly	Leu	Arg	Val	Glu	Arg	Leu	Arg	Pro	Val	Ala	180	185	190	
Ala	Val	Glu	Asn	Leu	His	Arg	Gly	Ser	Gln	Arg	Ala	Asp	Gly	Arg	Val	195	200	205	
Phe	Arg	Pro	Ile	Arg	Arg	Gly	Ala	Arg	Leu	Pro	Ala	Arg	Arg	Ser	Arg	210	215	220	
Ala	Gly	Pro	Gln	Gly	Arg	Leu	His	Leu	Asp	Gly	Ala	Gly	Pro	Ser	Pro	225	230	235	240
Leu	Pro	Ala	Arg	Ala	Gly	Gln	Gln	Gln	Pro	Ser	Ser	Ala	Gly	Gly	Arg	245	250	255	
Arg	Ala	Gly	Gly	Ala	Glu	Arg	Ala	Asp	Pro	Gly	Gln	Arg	Gly	Arg	His	260	265	270	
His	Gln	Gly	Gly	His	Asp	Pro	Gly	Arg	Gln	Gly	Ala	Gln	Arg	Gly	Thr				

275 280 285
 Ala Gly Val Ala His Ala Ala Ala Gly Pro Arg Arg Ala Ala Val Arg
 290 295 300
 Asn Arg Pro Arg Arg
 305

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 580 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ser Ala Val Trp Cys Leu Asn Gly Phe Thr Gly Arg His Arg His Gly
 1 5 10 15
 Arg Cys Arg Val Arg Ala Ser Gly Trp Arg Ser Ser Asn Arg Trp Cys
 20 25 30
 Ser Thr Thr Ala Asp Cys Cys Ala Ser Lys Thr Pro Thr Gln Ala Ala
 35 40 45
 Ser Pro Leu Gln Arg Arg Phe Thr Cys Cys Ser Pro Ala Val Gly Cys
 50 55 60
 Arg Phe Arg Ser Phe Pro Val Arg Arg Leu Ala Leu Gly Ala Arg Thr
 65 70 75 80
 Ser Arg Thr Leu Gly Val Arg Arg Thr Leu Ser Gln Trp Asn Leu Ser
 85 90 95
 Pro Arg Ala Gln Pro Ser Cys Ala Val Thr Val Glu Ser His Thr His
 100 105 110
 Ala Ser Pro Arg Met Ala Lys Leu Ala Arg Val Val Gly Leu Val Gln
 115 120 125
 Glu Glu Gln Pro Ser Asp Met Thr Asn His Pro Arg Tyr Ser Pro Pro
 130 135 140
 Pro Gln Gln Pro Gly Thr Pro Gly Tyr Ala Gln Gly Gln Gln Thr
 145 150 155 160
 Tyr Ser Gln Gln Phe Asp Trp Arg Tyr Pro Pro Ser Pro Pro Gln
 165 170 175
 Pro Thr Gln Tyr Arg Gln Pro Tyr Glu Ala Leu Gly Gly Thr Arg Pro
 180 185 190
 Gly Leu Ile Pro Gly Val Ile Pro Thr Met Thr Pro Pro Gly Met
 195 200 205
 Val Arg Gln Arg Pro Arg Ala Gly Met Leu Ala Ile Gly Ala Val Thr
 210 215 220
 Ile Ala Val Val Ser Ala Gly Ile Gly Gly Ala Ala Ala Ser Leu Val
 225 230 235 240
 Gly Phe Asn Arg Ala Pro Ala Gly Pro Ser Gly Gly Pro Val Ala Ala
 245 250 255
 Ser Ala Ala Pro Ser Ile Pro Ala Ala Asn Met Pro Pro Gly Ser Val
 260 265 270
 Glu Gln Val Ala Ala Lys Val Pro Ser Val Val Met Leu Glu Thr
 275 280 285
 Asp Leu Gly Arg Gln Ser Glu Glu Gly Ser Gly Ile Ile Leu Ser Ala
 290 295 300
 Glu Gly Leu Ile Leu Thr Asn Asn His Val Ile Ala Ala Ala Lys

```

305          110          115          320
Pro Pro Leu Gly Ser Pro Pro Pro Lys Thr Thr Val Thr Phe Ser Asp
          325          330          335
Gly Arg Thr Ala Pro Phe Thr Val Val Gly Ala Asp Pro Thr Ser Asp
          340          345          350
Ile Ala Val Val Arg Val Gln Gly Val Ser Gly Leu Thr Pro Ile Ser
          355          360          365
Leu Gly Ser Ser Ser Asp Leu Arg Val Gly Gln Pro Val Leu Ala Ile
          370          375          380
Gly Ser Pro Leu Gly Leu Glu Gly Thr Val Thr Thr Gly Ile Val Ser
          385          390          395
Ala Leu Asn Arg Pro Val Ser Thr Thr Gly Glu Ala Gly Asn Gln Asn
          405          410          415
Thr Val Leu Asp Ala Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn
          420          425          430
Ser Gly Gly Ala Leu Val Asn Met Asn Ala Gln Leu Val Gly Val Asn
          435          440          445
Ser Ala Ile Ala Thr Leu Gly Ala Asp Ser Ala Asp Ala Gln Ser Gly
          450          455          460
Ser Ile Gly Leu Gly Phe Ala Ile Pro Val Asp Gln Ala Lys Arg Ile
          465          470          475
Ala Asp Glu Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly
          485          490          495
Val Gln Val Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu
          500          505          510
Val Val Ala Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val
          515          520          525
Val Val Thr Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu
          530          535          540
Val Ala Ala Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr
          545          550          555
Phe Gln Asp Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly
          565          570          575
Lys Ala Glu Gln
          580

```

(2) INFORMATION FOR SEQ ID NO:76:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Leu Val Val Leu
1          5          10          15
Gly Ala Cys Leu Ala Leu Trp Leu Ser Gly Cys Ser Ser Pro Lys Pro
20          25          30
Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro
35          40          45
Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala Thr Lys Gly Leu
50          55          60
Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Leu

```


65	70	75	80
Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala Asn Pro Leu Ala			
	85	90	95
Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly Val Pro Phe Arg			
	100	105	110
Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp Asp Trp Ser Asn			
	115	120	125
Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val Leu Asp Pro Ala			
	130	135	140
Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn Leu Gln Ala Gln			
	145	150	155
Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys Ile Thr Gly Thr			
	165	170	175
Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly Ala Lys Ser Ala			
	180	185	190
Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser His His Leu Val			
	195	200	205
Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln Leu Thr Gln Ser			
	210	215	220
Lys Trp Asn Glu Pro Val Asn Val Asp			
225	230		

(2) INFORMATION FOR SEQ ID NO:77:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala		
1	5	10
Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val		
	20	25
Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile		
	35	40
Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln		
	50	55
Pro Arg		60
65		

(2) INFORMATION FOR SEQ ID NO:78:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Val Pro Pro Ala Pro Pro Leu Pro Pro Leu Pro Pro Ser Pro Ile Ser		
1	5	10
		15

Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala
 20 25 30
 Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Pro
 35 40 45
 Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro
 50 55 60
 Ser Pro Pro Leu Pro
 65

(2) INFORMATION FOR SEQ ID NO:79:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
 1 5 10 15
 Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
 20 25 30
 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 35 40 45
 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 50 55 60
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285

Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 Pro Pro Ala
 355

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ser Pro Lys Pro Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr
 1 5 10 15
 Ala Ser Asp Pro Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala
 20 25 30
 Thr Lys Gly Leu Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys
 35 40 45
 Val Asp Ser Leu Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala
 50 55 60
 Asn Pro Leu Ala Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly
 65 70 75 80
 Val Pro Phe Arg Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp
 85 90 95
 Asp Trp Ser Asn Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val
 100 105 110
 Leu Asp Pro Ala Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn
 115 120 125
 Leu Gln Ala Gln Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys
 130 135 140
 Ile Thr Gly Thr Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly
 145 150 155 160
 Ala Lys Ser Ala Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser
 165 170 175
 His His Leu Val Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln
 180 185 190
 Leu Thr Gln Ser Lys Trp Asn Glu Pro Val Asn Val Asp
 195 200 205

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
 1 5 10 15
 Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Glu
 20 25 30
 His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
 35 40 45
 Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
 50 55 60
 Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
 65 70 75 80
 Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
 85 90 95
 Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
 100 105 110
 Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
 115 120 125
 Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
 130 135 140
 Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
 145 150 155 160
 Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
 165 170 175
 Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
 180 185 190
 Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
 195 200 205
 Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
 210 215 220
 Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
 225 230 235 240
 Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
 245 250 255
 Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
 260 265 270
 Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys
 275 280 285

(xii) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr
 1 5 10 15
 Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp
 20 25 30
 Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg

111

```

      35              40              45
Asn His Ala Met Met Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg
 50              55              60
Val Glu Ile Pro Gly Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro
 65              70              75              80
Arg Glu Ala Leu Ala Leu Ala Leu Asp Gln Glu Arg Thr Val Thr Asp
      85              90              95
Gln Val Gly Arg Leu Thr Ala Val Ala Arg Asp Glu Gly Asp Phe Leu
      100              105              110
Gly Glu Gln Phe Met Gln Trp Phe Leu Gln Glu Gln Ile Glu Glu Val
      115              120              125
Ala Leu Met Ala Thr Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn
      130              135              140
Leu Phe Glu Leu Glu Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro
      145              150              155              160
Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu
      165              170

```

(2) INFORMATION FOR SEQ ID NO:83:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

Arg Ala Asp Glu Arg Lys Asn Thr Thr Met Lys Met Val Lys Ser Ile
 1              5              10              15
Ala Ala Gly Leu Thr Ala Ala Ala Ala Ile Gly Ala Ala Ala Gly
      20              25              30
Val Thr Ser Ile Met Ala Gly Gly Pro Val Val Tyr Gln Met Gln Pro
      35              40              45
Val Val Phe Gly Ala Pro Leu Pro Leu Asp Pro Xaa Ser Ala Pro Xaa
      50              55              60
Val Pro Thr Ala Ala Gln Trp Thr Xaa Leu Leu Asn Xaa Leu Xaa Asp
      65              70              75              80
Pro Asn Val Ser Phe Xaa Asn Lys Gly Ser Leu Val Glu Gly Gly Ile
      85              90              95
Gly Gly Xaa Glu Gly Xaa Xaa Arg Arg Xaa Gln
      100              105

```

(2) INFORMATION FOR SEQ ID NO:84:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

Val Leu Ser Val Pro Val Gly Asp Gly Phe Trp Xaa Arg Val Val Asn
 1              5              10              15
Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr

```

412

		20								25									30
Arg	Arg	Ala	Leu	Glu	Leu	Gln	Ala	Pro	Ser	Val	Val	Xaa	Arg	Gln	Gly				
		35																	
Val	Lys	Glu	Pro	Leu	Xaa	Thr	Gly	Ile	Lys	Ala	Ile	Asp	Ala	Met	Thr				
		50					55												
Pro	Ile	Gly	Arg	Gly	Gln	Arg	Gln	Leu	Ile	Ile	Gly	Asp	Arg	Lys	Thr				
		65				70					75								
Gly	Lys	Asn	Arg	Arg	Leu	Cys	Arg	Thr	Pro	Ser	Ser	Asn	Gln	Arg	Glu				
					85					90									
Glu	Leu	Gly	Val	Arg	Trp	Ile	Pro	Arg	Ser	Arg	Cys	Ala	Cys	Val	Tyr				
			100						105										
Val	Gly	His	Arg	Ala	Arg	Arg	Gly	Thr	Tyr	His	Arg	Arg							
		115					120					125							

(2) INFORMATION FOR SEQ ID NO:85:

(4) SEQUENCE CHARACTERISTICS.

- (A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:85.

Cys Asp Ala Val Met Gly Phe Leu Gly Gly Ala Gly Pro Leu Ala Val
 1 5 10 15
 Val Asp Gln Gln Leu Val Thr Arg Val Pro Gln Gly Trp Ser Phe Ala
 20 25 30
 Gln Ala Ala Val Pro Val Val Phe Leu Thr Ala Trp Tyr Gly Leu
 35 40 45
 Ala Asp Leu Ala Glu Ile Lys Ala Gly Glu Ser Val Leu Ile His Ala
 50 55 60
 Gly Thr Gly Gly Val Gly Met Ala Ala Val Gln Leu Ala Arg Gln Trp
 65 70 75 80
 Gly Val Glu Val Phe Val Thr Ala Ser Arg Gly Lys Trp Asp Thr Leu
 85 90 95
 Arg Ala Xaa Xaa Phe Asp Asp Xaa Pro Tyr Arg Xaa Phe Pro His Xaa
 100 105 110
 Arg Ser Ser Xaa Gly
 115

(2) INFORMATION FOR SEQ ID NO: 86:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Tyr Arg Phe Ala Cys Arg Thr Leu Met Leu Ala Ala Cys Ile Leu
1 5 10 15
Ala Thr Gly Val Ala Gly Leu Gly Val Gly Ala Gln Ser Ala Ala Gln
20 25 30

```

Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp
  35                                40                                45
Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asp Phe
  50                                55                                60
His Arg Asp Ser Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro
  65                                70                                75
Ile Leu Glu Gly Pro Val Leu Asp Asp Pro Gly Ala Ala Pro Pro Pro
  80                                85                                90
Pro Ala Ala Gly Gly Gly Ala
  100

```

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```

Val Gln Cys Arg Val Trp Leu Glu Ile Gln Trp Arg Gly Met Leu Gly
  1                                5                                10
Ala Asp Gln Ala Arg Ala Gly Gly Pro Ala Arg Ile Trp Arg Glu His
  15                                20                                25
Ser Met Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala
  30                                35                                40
Thr Lys Glu Gly Arg Gly Ile Val Met Arg Val Pro Leu Glu Gly Gly
  45                                50                                55
Gly Arg Leu Val Val Gln Leu Thr Pro Asp Glu Ala Ala Ala Leu Gly
  60                                65                                70
Asp Glu Leu Lys Gly Val Thr Ser
  75                                80

```

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
  1                                5                                10
Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
  15                                20                                25
Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
  30                                35                                40
Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
  45                                50                                55
Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
  60                                65                                70
Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
  75                                80

```

114

85

90

95

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
1      5      10      15
Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
20      25      30
Pro Ile Thr Pro Cys Glu Leu Thr Xaa Xaa Lys Asn Ala Ala Gln Gln
35      40      45
Xaa Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
50      55      60
Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Xaa
65      70      75      80
Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
85      90      95
Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
100      105      110
Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
115      120      125
Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
130      135      140
Gln Gly Ala Ser Leu Ala His Xaa Gly Asp Gly Trp Asn Thr Xaa Thr
145      150      155      160
Leu Thr Leu Gln Gly Asp
165

```

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```

Arg Ala Glu Arg Met
1      5

```

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```

Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
1      5      10      15
Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
20      25      30
Val Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
35      40      45
Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
50      55      60
Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Met Phe
65      70      75      80
Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
85      90      95
Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
100     105     110
Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
115     120     125
Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
130     135     140
Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
145     150     155     160
His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
165     170     175
Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
180     185     190
Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr Ala
195     200     205
Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
210     215     220
Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
225     230     235     240
Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
245     250     255
Arg Arg Asn Gly Gly Pro Ala
260

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(2) INFORMATION FOR SEQ ID NO:92:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala
1      5      10      15
Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Glu Gly
20      25      30
Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly
35      40      45
Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr

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50	55	60
Glu Leu Gly Gly Gly Asp Gly Ala Val Ser Gly Asp Thr Gly Leu Pro		
65	70	75
Val Gly Val Ala Leu Leu Ala Ala Leu Ala Gly Val Val Leu Val		80
	85	90
Pro Lys Ala Lys Ser Met Val Thr Val Val Ala Val Leu Gly Val Leu		95
	100	105
Gly Val Phe Leu Met Val Ser Ala Thr Phe Asn Lys Pro Ser Ala Tyr		110
	115	120
Ser Thr Gly Trp Ala Leu Trp Val Val Leu Ala Phe Ile Val Phe Gln		125
	130	135
Ala Val Ala Ala Val Leu Ala Leu Leu Val Glu Thr Gly Ala Ile Thr		140
	145	150
Ala Pro Ala Pro Arg Pro Lys Phe Asp Pro Tyr Gly Gln Tyr Gly Arg		155
	160	165
Tyr Gly Gln Tyr Gly Gln Tyr Gly Val Gln Pro Gly Gly Tyr Tyr Gly		170
	175	180
Gln Gln Gly Ala Gln Gln Ala Ala Gly Leu Gln Ser Pro Gly Pro Gln		185
	190	195
Gln Ser Pro Gln Pro Pro Gly Tyr Gly Ser Gln Tyr Gly Tyr Ser		200
	205	210
Ser Ser Pro Ser Gln Ser Gly Ser Gly Tyr Thr Ala Gln Pro Pro Ala		215
	220	225
Gln Pro Pro Ala Gln Ser Gly Ser Gln Gln Ser His Gln Gly Pro Ser		230
	235	240
Thr Pro Pro Thr Gly Phe Pro Ser Phe Ser Pro Pro Pro Val Ser		245
	250	255
Ala Gly Thr Gly Ser Gln Ala Gly Ser Ala Pro Val Asn Tyr Ser Asn		260
	265	270
Pro Ser Gly Gly Glu Gln Ser Ser Ser Pro Gly Gly Ala Pro Val		275
	280	285
	290	295
		300

(2) INFORMATION FOR SEQ ID NO:93:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Gly Cys Gly Glu Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn	
1	5
Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile	10
	15
	20
	25

(2) INFORMATION FOR SEQ ID NO:94:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Gly Cys Gly Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala
 1 5 10 15
 Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
 20 25

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Gly Cys Gly Gly Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu
 1 5 10 15
 Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu
 20 25

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Gly Cys Gly Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr
 1 5 10 15
 Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
 20 25

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids

118

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Gly Cys Gly Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu
 1 5 10 15
 Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 20 25

(2) INFORMATION FOR SEQ ID NO:99:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 507 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGAAGATGG TGAATCGAT CCGCCAGGT CTGACCCCG CGGCTGCAAT CCGGCCCGCT 60
 GCGGCCGGTG TGAATCGAT CATGCTGCG GCGCCGCTG TATACGAGAT GCAGCCCGTC 120
 GTCTTGGCGG CGCCTACTGCC GTTGGACCG GCATCGGCC CTGACTTCCC GACCGCCGCC 180
 CAGTTGACCA GCGTCTCAA CAGCTTCGG GATCCCAAC TGTCTTTTC GAACAAAGGC 240
 AGTCTGCTCG AGGGCGGAT CCGGCGCAC GAGGCGCGCA TCGCCGACCA CAAGCTGAAG 300
 AAGCCCGCC AGCACGGGA TGTGCGGCT TCTTCACGC TGACGAACAT CCAGCCCGCG 360
 GCGCCCGGTT CCGCCACCG CAGCTTTTC GTCTCGGTC CGAAGCTTC GTCCCGGTC 420
 ACGCAGAAC TCAGCTTCG GAATCAAGGC GCGTGGATG TGTACGCGC ATCGGCGATG 480
 GAGTTGCTTC AGGCGGAGG GAATGA 507

(2) INFORMATION FOR SEQ ID NO:100:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala Ala Ala Ala
 1 5 10 15
 Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala Gly Gly Pro
 20 25 30
 Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro Leu Pro Leu
 35 40 45
 Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
 50 55 60
 Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn Lys Gly
 65 70 75 80
 Ser Leu Val Gln Gly Gly Ile Gly Gly Thr Glu Ala Arg Ile Ala Asp
 85 90 95
 His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro Leu Ser Phe

	100		105		110										
Ser	Val	Thr	Asn	Ile	Gln	Pro	Ala	Ala	Gly	Ser	Ala	Thr	Ala	Asp	
	115		120		125										
Val	Ser	Val	Ser	Gly	Pro	Lys	Leu	Ser	Ser	Pro	Val	Thr	Gln	Asn	Val
	130		135		140										
Thr	Phe	Val	Asn	Gln	Gly	Gly	Trp	Met	Leu	Ser	Arg	Ala	Ser	Ala	Met
	145		150		155									160	
Glu	Leu	Leu	Gln	Ala	Ala	Gly	Asn								
			165												

(2) INFORMATION FOR SEQ ID NO:101:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(3) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CGTGGCAATG	TGGTTGACCG	TGGGGGGCGG	GGTGCCTCC	GCAGATCCCG	TGGACGGGGT	60
CATTACACC	ACCTGCAATT	ACGGGCGAGT	AGTAGCTGCC	CTCAACGCGA	CGGATCCGGG	120
GGCTGCCCGA	CAGTTCAAGC	CCTCACCAGT	GGCGAGTCC	TATTTCGCGA	ATTTCCTGCG	180
CGCACCGCGA	CCTCAGCGCG	CTCCATGGCG	CGCGCAATTC	CAGCTCTGCG	CGGGGGCGGC	240
ACAGTACATC	GGCCTTGTGG	AGTCGGTTGC	CGGCTCTGCG	AACACTATT	AAGCCCATGC	300
GGGCTTCATC	CGCGACCGCG	GCATGCTGCG	CGGGGCTAGG	CCAGATTGCC	CGGCTCTCCA	360
ACGGGCGCGA	TCCGCGAGCG	CGGCATGCTC	CCCGGGGCTA	GGCCAGATTG	CCCGCTCTCT	420
CACCGGCGCG	CATCTGCTGC	CGAATCTGCG	CAGCCCGGGG	GATCCACTAG	TTCTAGAGCG	480
GGCGGCGCGG	CGGTGGAGCT					500

(2) INFORMATION FOR SEQ ID NO:102:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(3) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Val	Ala	Met	Ser	Leu	Thr	Val	Gly	Ala	Gly	Val	Ala	Ser	Ala	Asp	Pro
1				5					10				15		
Val	Asp	Ala	Val	Ile	Asn	Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val	Val	Ala
			20					25				30			
Ala	Leu	Asn	Ala	Thr	Asp	Pro	Gly	Ala	Ala	Ala	Gln	Phe	Asn	Ala	Ser
			35				40				45				
Pro	Val	Ala	Gln	Ser	Tyr	Leu	Arg	Asn	Phe	Leu	Ala	Ala	Pro	Pro	Pro
			50			55				60					
Gln	Arg	Ala	Ala	Met	Ala	Ala	Gln	Leu	Gln	Ala	Val	Pro	Gly	Ala	Ala
			65			70				75				80	
Gln	Tyr	Ile	Gly	Leu	Val	Glu	Ser	Val	Ala	Gly	Ser	Cys	Asn	Asn	Tyr
					85				90					95	

(2) INFORMATION FOR SEQ ID NO:103:

(4) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(XX) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGACAGAGC AGCAGTGGAA TTTCGCGGOT ATCGAGGCGG CGGCAAGCGC AATCCAGGGA 60
AATGTACGCT CCAITCATTC CTTCTTTGAC GAGGGGAGGC AGTCCCTGAC CAAGCTCGCA 120
GCGGCTTGGG GCGGTAGCGG TTCCGAAGCG TACC 150

(2) INFORMATION FOR SEQ ID NO:104:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:104:

[illegible]

(2) INFORMATION FOR SEQ ID NO:106:

(5) SEQUENCES CHARACTERISTICS.

- (A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(XXI) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CGTTCGCGCA	CTTCAGGTG	ACTATGAAG	TGGGCTTCGG	CTGGAGAGAT	TCCTGACCT	60
TCAAGCGCGG	CGATACGTG	AGGTGCATCA	TTAAGGGAAT	TTTCCAGAC	ATCTGACGC	120
GCTCGAAAG	CGGCACAGCG	AGCTGTGGCT	CCGCGAGAGC	GCTTGTCTCA	AAATCCCTGA	180
SACCTATCGN	CGGGGCGCGC	TACAGGAAG	TGGTGTCTGA	ATTCGCGNG	TATCTGGTCG	240
ACCTGTGTGG	TCTGAGCTG	GACGAAGCG	TGCTCTGAT	CG		282

(2) INFORMATION FOR SEQ ID NO:106:

(2) SEQUENCE CHARACTERISTICS.

- (A) LENGTH: 3058 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATCGTACCC GTGCGAGTGC TCGGCGCSTT TGAAGATGGA GTGCACGTGT CTTTCGTGAT	60
GGCATACCCA GAGATGTTGG CGCGCGCGCG TGACACCCCTG CAGAGCATCG GTGCTACCAAC	120
TGTGGCTAGC AATGCCGCTG CGCGCGCGCC GACGACTGGG GTGGTGCCCC CCGCTGCCGA	180
TGAGGTGTGC GCGCTGACTG CGCGCGCACTT CGCGCGCATAT GCGGCGATGT ATCAGTCCGT	240
GAGCGCTCGG GCTGCTGCGA TTCATGACCA GTTCGTGGCC ACCCTTGCCA GCAGCGCGAG	300
CTCGTATGCG GCCACTGAAG TGCCCAATGC GCGCGCGCGC AGCTAAGCCA GGAACAGTCG	360
GCACGAGAAA CCACGAGAAA TAGGACACCG TAATGCTGGA TTTCGGGCGG TTACCAACCG	420
AGATCAACTC CGCAGAGATG TACCGCGGCC CGGGTTCGGC CTCGCTGGTG GCGCGCGCTC	480
AGATGTGGGA CAGCTGGCGG AATGACCTGT TTTCGGCGCG CTCGCGCTTT CAGTCGGTGG	540
TCTGGGCTCT GACGCTGGGG TCGTGATAG GTTCGTCCGC GGGTCGTGAT GTGCGCGCGG	600
CCTCGCGCTA TTGCGCTGG ATGAGCGTCA CGCGCGCGCA GCGGAGCTG ACCGCGCGCC	660
AGGTCCGGGT TGCTCGCGCG GCTTACGAGA CGCGTATGCG GCTGACGGTG CCGCGCGCGG	720
TGATCGCGGA GAACCTGCTT GAAGTATGA TTCTGATAGC GACCAACCTC TTGGGGCAAA	780
ACACCGCGCG GATCGCGTTC AACGAGCGCG AATACCGCGA GATGTGGGCC CAAGACGCGG	840
CGCGCATGTT TGGCTAGGCT GCGCGGACCG CGAGCGGAC GCGGACGTTG CTCGCGTTGG	900
AGGAGCGCGC GAGATGACC AGCGCGCGTG GCGCTCTGGA GCAGGCGCGC GCGGTGGAAG	960
AGCGCTGCGA CACCGCGCGG CGGAACCACT TGATGAACAA TTGCGCGCAG GCGCTGCAAC	1020
AGCTGCGCCA GCGGCGCGAG GGCACCGCGC GTTCTTCCAA GCTGCTGCGC CTGTGGAAGA	1080
CGGTCTGCGC GCATCGCTCG CGGATCAGCA ACATGCTGTC GATGCGCAAC AACGACATGT	1140
CGATGACCAA CTCGGGTGTG TCGATGACCA ACACCTTGAG CTCGATGTTG AAGGCTTTTG	1200
CTCGCGCGCG GCGCGCTCAG GCGGTGCAAA CCGCGCGCGA AAACGGGGTC CGGGCGATGA	1260
GCTCGCTGGG CAGCTCGCTG GGTTCCTCGG GTCTGGGCGG TGGGTTGGCC GCCAAGCTGG	1320
GTGCGCGCGC CTCGCTCGGT TCGTGTGCGG TGCGCGAAGC CTGGGCGCGG GCCAAGCAGG	1380
CAGTCACCCC GCGCGCGCGG GCGCTGCGCG TGACCAAGCT GACCAAGCCC GCGGAAGAG	1440
GGCGCGCGCA GATGCTGGCG GCGCTGCGCG TGGGCGAGAT GGGGCGCAGG GCGGCTGCTG	1500
GGCTCAGTGG TGTGCTGCGT GTTGCGCGCG GACCTATGAT GATGCGCGAT TCTCGCGCGG	1560
CGGCTAGGGA GAGGCGCGCG AGACTGTGCT TATTTGACCA GTGATGCGCG GTCTCGGTGT	1620

TTCCGCGGCC	GGCTATGACA	ACAGTCAATG	TGCATGACAA	GTTACAGGTA	TTAGGTCCAG	1580
GTTCAACAAG	GAGACAGGCA	ACATGGGCTC	ACGTTTTATG	ACGGATCCGC	ACCGGATGCG	1740
GGACATGGCG	GGCGTTTTG	AGGTGCACGC	CCAGACGGTG	GAGGACUAGG	CTCGCCGGAT	1800
GTGGGCGTCC	GGCAAAACA	TTTCCGGTGC	GGGCTGGAGT	GGCATGGCCG	AGCGGACCTC	1860
GCTAGACACC	ATGGCCGAGA	TGAATCAGGC	GTTTCGCAAC	ATCGTGAACA	TGCTGCACGG	1920
GGTGGGTGAC	GGGCTGGTTC	GCGACGCCAA	CAACTACGAG	CAGCAAGAGC	AGGGCTCCCA	1980
GCAGATCCTC	AGCAGCTAAC	GTGAGCGGCT	GCAGCACAA	ACTTTTACAA	GCGAAGGAGA	2040
ACAGGTTGGA	TGACCATCAA	CTATCAATTC	GGGGATGTGG	ACGGTCACGG	CGCGCTGATC	2100
CGGCTCAGG	CCGGGTTCCT	GGAGGCGGAG	CATCAGGCCA	TCATTCTGGA	TGCTTACACC	2160
GCGAGTGAAT	TTTGGGGCGG	GGCGGGTTCG	GCGGCGTGCC	AGGGGTTGAT	TACCCAGTTG	2220
GGCGCTAACT	TCCAGGTGAT	CTACGAGCAG	GCCAACGCCC	ACGGGCGAGA	GGTGCAGGGT	2280
GCCTGCAACA	ACATGGGCCA	AACCGACAGC	GCCTCGGCT	CCAGCTGGGC	CTGACACGAG	2340
GCCAAGGCCA	GGGACGTGGT	GTACGAGTGA	AGTTCCTCGC	GTGATCTCTC	GGGTGGCAAT	2400
CTAAGTGGTC	AGTCTCGGG	TGTTGGTGGT	TTGCTGCTTG	GCGGTTCTCT	CGGTGCTGGT	2460
CAGTGTCTCT	GGGGCTGGGG	TGAGGACCTC	GAAGGCCAGG	TAGCGCCGTC	CTTGATCTCA	2520
TTCTGTGTGT	TGTTGGGCGA	GGACGGCTCC	GACGAGCGCG	ATGATCGAGG	CGCGGTGGGG	2580
GAAGATGCCC	ACGACGTCCG	TTGCGGCGTG	TACCTCTGCG	TTGAGGCGGT	CGTGGGGTT	2640
GTGAGACCGG	ATTTGGCCGC	AGAICTGCTT	GGGGAAGGCG	GTGAACGCCA	GCAGGTGGGT	2700
GCGGGCGGTC	TGAGGTGCT	CGGCCACCGC	GGGAGTTTG	TCCGTCAGAG	CGTCAGATAC	2760
CCGATCATAT	TGGGCAACAA	CTGATTCGCG	GTGCGGCTGG	TCTAGATGCG	AGTGCACGAG	2820
GGTGGGCACT	CACGCGGAGG	AGGGCTTCGG	GCTGGCTGCG	ATCAGATTGG	CTGCTAGTGG	2880
GTTTCTGCGA	GCTTCCGAGG	TCGCTGGCGG	CAGGGTGGCG	CCGATCGCGG	CCACCAGGCG	2940
GGCGTGGCGG	TGCTGTGTA	CCAGCGCGAC	CCCGACACGG	CGCGGGGCGA	CCAGGTCCGG	3000
GAAGAAGGCC	AGCCAGCGGG	CCCGCTCTCT	GGCGGAGGTC	ACCTGGATGC	CCAGGATC	3058

(2) INFORMATION FOR SEQ ID NO:107:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15

Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
 20 25 30

Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60

Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80

Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95

Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110

Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
 115 120 125

Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
 130 135 140

Trp Ala Gln Asp Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
 145 150 155 160

Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
 165 170 175

Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
 180 185 190

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205

Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
 210 215 220

Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
 225 230 235 240

Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
 245 250 255

Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
 260 265 270

124

Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
275 280 285

Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
290 295 300

Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
305 310 315 320

Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
325 330 335

Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
340 345 350

Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
355 360 365

Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
370 375 380

Pro His Ser Pro Ala Ala Gly
385 390

(2) INFORMATION FOR SEQ ID NO:108:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1725 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(21) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GACGTCAGCA	CCGCGCTGTC	AGGCGTGGAG	CGTGGTCGGT	TTTGATCTGC	GGTCAGGTG	60
ACGTCCCTCG	GGGTGTGCCC	GGCGTGATG	CAGACTCGAT	GGCGTCTCTT	AGTGCACTA	120
ATTTCCTTGA	AGTGCTCTGG	AGGTATAGGA	CTTCACGATT	GGTTAAGSTA	GGCTTCACCC	180
CGTGTGTGGG	TGATTTGGC	CGGACCACTC	GTACCAACAG	CTTGGCGTGC	GGCGCAGCGG	240
GGCGATCAGA	TGGCTTGACT	ACCAATCAAT	CTTGAGCTCC	CGGCGCGATG	CTCGGCGCTAA	300
ATGAGCAGGA	GCACGCTGT	CTTTCACCTG	GCAACCGGAG	ATGTTGGCGG	CGCGCGCTGG	360
CGACTTCTCT	TGCTGTGGGG	CAACCGTGAA	GGCTAGCAAT	GGCGCGCGAG	CGGTGCGGAC	420
GACTGGGGTG	GTGCCCCCGG	CTGCGGACGA	GGGTGTGGCTG	CTGCTTGCCA	CACRATTCCG	480
TACGCATGCG	GGGACGTATC	AGACGGCGAG	CGGCAAGGCC	GGGTGATGTC	ATGAGCAGTT	540
TGTGACCAAG	CTGGCCACUA	GGCTAGCTTC	ATATGCGGAC	ACCGAGGCGG	CCAACGCTGT	600
GGTCACCGGC	TAGCTGACTC	GAGCGTATTC	GAGCGGAAGG	ATTATCGAAG	TGCTGGGATT	660

CCGGGCGCTTA CCACCGGAGA TCAACTCCGC GAGGATGTAC GCGGCGCCGG GTTCGGCCTC 720
 GCTGGTGGCC GCGCGGAAGA TGTGGGACAG CGTGGCGAGT GACCTGTTTT CGGCGCCGTC 780
 GCGGTTTCAG TCGTUGTCT GGGGCTGAC GGTGGGCTCG TGGATAGTT CGTGGCGGG 840
 TGTGATGGCG GCGCGGGCCT CGCGTATGT GCGGTGATG AGCGTCACCG CCGGCGAGGC 900
 CCACTGACCC GCGCGCCAGG TCGGGGTTCG TCGGCGCGCC TACGAGACAG CGTATAGGCT 960
 GACGGTGGCC CCGCGCGTGA TCGCGGAGAA CGGTACCGAA CTGATGACGC TGACCGGAC 1020
 CAACCTCTTG GCGCAAAACA CCGCGGCGAT CAGGCGCAAT CAGCGCGCAT ACAGCGAGAT 1080
 GTGGGGCCAA GACCGGAGG CGATGTATGG CTACCGCCGC ACGCGGGCGA CCGCGACCGA 1140
 GCGCTTGCTG CGCTTGAGG AGCGCCGACT GATCACCAAG CCGCGCGGGC TCGTTGAGCA 1200
 GCGCGTGGCG GTGAGGAGG CCGTGGACAC CCGCGCGGGC AAGCGTTGTA TGAACAAATG 1260
 GCGCCAAAGC CTGCAACAGC TCGCGCGCC AGCGGAGGCG GTGCTACCTT CTTCGAGCT 1320
 GGTGCGGCTG TGGAGCGCG TGTGCGCGCA TGTGTGCGCG CTCAGCAAGC TCAGTTGAGT 1380
 AGCGAACAAC CACATGTGGA TGATGCGCAC GGGTGTGTG ATGACCAACA CTTGCACTC 1440
 GATGTTGAGG GGTTAGCTC CCGCGCGGGC TCGGCGCGTG GAAACCGCG CCGAACAAG 1500
 GTGTGCGCG ATGAGCTGC TCGGCGAGCA GCTGGGTTG TCGTGGGTT CTTCGGGCT 1560
 GGGCGCTGGG GTGGCGGCA ACTTGGGTG GCGCGCGTGG GTCGGTTGT TGTGGGTGC 1620
 GCGAGCATG GCGCGCGCA ACCAGGCGGT CACCGCGCG GCGCGCGCG TCGCGGTGAC 1680
 CAGCTGACC AGCGCGCGCC AAACCGCGCC CCGACACATG CTGGG 1725

(2) INFORMATION FOR SEQ ID NO:109:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1725 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ix) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15
 Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Lys Met Trp
 20 25 30
 Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60
 Leu Met Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80
 Ala Gly Gln Ala Gln Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95
 Ala Tyr Glu Thr Ala Tyr Arg Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110
 Glu Asn Arg Thr Glu Leu Met Thr Leu Thr Ala Thr Asn Leu Leu Gly
 115 120 125
 Gln Asn Thr Pro Ala Ile Glu Ala Asn Gln Ala Ala Tyr Ser Gln Met
 130 135 140
 Trp Gly Gln Asp Ala Glu Ala Met Tyr Gly Tyr Ala Ala Thr Ala Ala
 145 150 155 160
 Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr
 165 170 175
 Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile
 180 185 190
 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205
 Gln Gln Leu Ala Gln Pro Ala Gln Gly Val Val Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Thr Ala Val Ser Pro His Leu Ser Pro Leu Ser Asn
 225 230 235 240
 Val Ser Ser Ile Ala Asn Asn His Met Ser Met Met Gly Thr Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu His Ser Met Leu Lys Gly Leu Ala Pro Ala
 260 265 270
 Ala Ala Gln Ala Val Glu Thr Ala Ala Glu Asn Gly Val Trp Ala Met
 275 280 285
 Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu
 290 295 300
 Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser
 305 310 315 320
 Leu Ser Val Pro Pro Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro
 325 330 335

Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr
 340 345 350

Ala Pro Gly His Met Leu Gly
 355

(2) INFORMATION FOR SEQ ID NO:110:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3027 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AGTTCACTGG AGAATGATAC TGACGGGGCTG TATCCACGAT GCGTGAGACA ACCGAACCAC	60
CGTCGGACGC GGGGACATCG CAAGCTGACG CGATGGCGTT GGGCGCGGAA GCGGAAGCGG	120
CGGAAGCGGA AGGGCTGGCC GCGGGGGGCG GGGCGCGTGC CGTTCGCGCC CGTTTGAASC	180
GTGAGCGCGT GCGGATGGCC CCAGCGGAGG ACAGAGACCT CCGCGAGGAT ATGCAGACTG	240
GGAGAGCGCT GAAGACTATG ACGACTATGA CGACTATGAG GCGCGAGACC AGGAGCGCGC	300
ACGGTCGCGA TCTTGCGACG GGGGGTGGG GGTGCGGTTA CCAAGACTGT CCACGATTGC	360
CATGGCGGCT CGATCTGCA TCATCTGCG GTTCACGGGG CTCAGCGGAT ACATTGTGTG	420
GCAACACCAT GAGGCGACCG AACGCGACCA GCGGCGCGCG GCGTTCGCGC CTGGAGCGCA	480
GCACGGTCTC ATCAACATGA CTTGCGTGGG CTTCAACAGG GCGAAGAAGG ACGTCGCGCG	540
TGTGATCGAC AGCTCCACCG GCGAATTGCG GATGACTTC CAGCAGCGCG CAGCGGATTT	600
CGCCAAAGTT CTCGAACAGT CCAAACTGGT CACCGAAGGC ACGGTGAACG CGACAGCGGT	660
CGAATCCATG AAGGAGCATT CCGCGGTGGT GCTGCTCGCG GCGACTTCAC GGTTCACCAA	720
TTCGCGTGGG GCGAAGACCG AACCACTGTC GTGCGCGCTC AAGATGACCG TGACCGAAGA	780
GGGGGACAGC TACAAGATGT CGAAAGTTGA GTTGCTACCG TGACCGATGA CTACCGCGAC	840
GTACACACCG AAACCACTGA CCGCACCGAA GTGCGTGA GA TCGACTCAGC CGCAGGCGAA	900
GCGGCTAATT GCGGACCGGA GGCATTGAC ACCGACTCTG CAACCGAATC TACCGCGCAG	960
AAGGCTCAGC CGCACCGTGA CCGTGGCGGA ATGCAGGTTA CTTTGAACCC CGTTCGCGTG	1020
ATTCTGATCC TGCTCATGTT GATCTCTGGG GCGCGACCG GATGGCTATA CTTTGAGCAA	1080
TACACCGGA TCAGCAGACG GACTCTGGCG CCGCGCTGTC TCGGTCGCGC GCGCGGTGTG	1140
ACGGGACAA CTGCGGTGTT TGTATTACCC CGACACCTCG ACCAGACTT CGCTACCGCC	1200

AGGTGGCACC TGGCGGGGGA TTCTCTGTCC TATACGACCA GTTCACGCAG CAGATCGTGG	1260
CTCCGGCGCG CAAACAGAAAG TCACTGAAAA CCAACCGCAA GGTGGTGCGC GCGGCCGTGT	1320
CGGAGCTACA TCGGATTTGG GCGGTGGTTC TGTTTTTTGT CGACCAAGAGC ACTACCACTA	1380
AGGACAGGCC CAATCGGTGG ATGGCGGCCA GCAGCGTGAT GGTGACCCCTA GCGAGGTGG	1440
ACGGCAATTG GGTGATCACC AAGTTCAACC CGGTTTAGGT TGCCGTAGGC GGTGCCCAAG	1500
TGTACCGGGG GCGCGGGTGG CTGCTCGTGC GAGATACGGG CGGTTCTCGG GACAATCAGC	1560
GCCCGACCTG AAACAGATCT CGGCGCTGTT CTAATCGGCC GGGTTATTTA AGATTAGTTG	1620
CCACTGTATT TACCTGATGT TCGATTGTT CAGCTGGATT TAGCTTCGCG GCGGGCGCGC	1680
TGGTGCACCT TGCATCTGGG GTTGCTACTA CTTGAGAGAA TTTGACCTGT TCGCGACGTT	1740
GTTTGCTGTC CATCATGGT GCTAGTTATG GCGGACCGGA AGGATTATCG AAGTGGTGGC	1800
CTTGCGGCGC TTACCAACCG AGATCAACTC CGGAGGATG TACGCCCGCC CGGGTTCGCG	1860
CTCGCTGGTG GCGCGCGGGA AGATGTGGGA CAGCGTGGCG AGTGACCTGT TTTCGGGCGC	1920
GTGGCGCTTT CAGTCGCTGG TGTGGGTTCT GACGACGGGA TGTGGGATAG GTTCGTCGCG	1980
GGGTGTGATG GTGGCGGCGG CTTGCGGGTA TGTGGCGTGG ATGAGCGTCA CGCGGGGGCA	2040
GGCGGAGCTG ACCCGCGCGC AGGTCCGGGT TGCTGCGGCG GCTACGAGA CGGCGTATGG	2100
GCTGACGTG CCGCGCGCGG TGATCGCCGA GAACGTGCT GAACGTGATGA TTCTGATAGC	2160
GACCAACCTC TTGGGGCAAA ACACCGCGCG GATCGCGTC AACGAGCGCG AATACGGGGA	2220
GATGTGGGCG CAAGACGGCG CGCGATGTT TGGCTACGCG GCCACGGCGG CGACGGCGAC	2280
CGAGCGCTTG CTGCGCTTGG AGGACGCGCG ACTGATCACC AAGCGCGCGG GGTCTCTTGA	2340
GKAGGCGCTG GCGGTGAGG AGGCCATCGA CACCGCGCGG GCGAACCGGT TGATGAACAA	2400
TGTGCGCCAA GCGGTGCAAC AACTGCGCCA GCGGACGAAA AGCATCTGGC CGTTCGACCA	2460
ACTGAGTGAA CTGTGAAAAG CCATCTCGCC GCATCTGTGG CGGCTCAGCA ACATCTGTTC	2520
GATGCTCAAG AACCACTGT CGATGACCAA CTGCGGTGTG TCGATGGCCA GCACTTCCA	2580
CTCAATCTTG AAGGGCTTGG CTGCGCGCGC GCGTCAGGCG GTGAAACCG CGGCGCAAAA	2640
CGGGTTCAG GCGATGAGCT CGCTGGCGAG CGAGCTGGGT TCGTCCCTGG GTTCTTCGGG	2700
TCTGCGGCTT GGGTGGCGCG CCAACTTGGG TCGGGCGGCC TCGGTCTGGT CGTTGTCTGG	2760
GCGGACGGCC TGGCGCGCGG CCAACGAGGC GGTCACTGCG GCGGCGGGGG CGCTGCGGCT	2820